

```

QY 512 NDHIGLEPREAVTIGEDVSGMPTVCIPVEDGGVGFDRYLHMAVADKWEIIOKREDEMK 571
DB 471 NSVSYSTPGLIISTAEESTSWPMVSMPTVVGIGFENLK-----WNM 511
QY 572 G---DIVMHLTRRLLEKCVSAESHDAVADKTIATFWMADKMDMALDRSTPLID 628
DB 512 GMMHMDLYFSMDPW-----FRQFHQNSI-----FFSMYHNSNY-MALASHDE----- 555
QY 629 RCVALHKKRILITMGLGGE--GYLN-----FMGNEFGH--PEWIDFPRG 668
DB 556 ---VHGKSNMIGKMPGDEMOKYAVRALFTYMFTHPGKKTFMSEMGQSEMWVW--G 610
QY 669 DLHDSGKFPVGNNSYDKCRRPDLGNSKHLRYHGMQEDQAIQHLBE-----AYGFM 722
DB 611 DLEMHLLNPPP-----HOOLKOFTELNLHYKNEBALYSNDFD 648
QY 723 TSEHGYISKDRDLIYPERGN-----LYPVFNHMTSSSDVRVGLCPKAKKIYLD 776
DB 649 ESGFWMIDCSDRHSHSVSTRRAKNSAEFVYTCNF--TPQPHSHRVGVPPVGFYTELFN 707
QY 777 SDDPLFGG--FGRLSHD--AEHSPFGWYDNRPSFMVYTPCTAVVVALVEDEVEN 829
DB 708 SPARYGGSNMGNLTGKWTWEMSFH-----EOPYSIDLCLPLSLVYLKLSQNAEEN 759

RESULT 8
GLGB_BACST STANDARD: PRT: 639 AA.
ID GLGB_BACST STANDARD: PRT: 639 AA.
AC P30538:
DR 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE 01-FEB-1995 (Rel. 31, Last annotation update)
DE 1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOGEN BRANCHING
ENZYME).
GN GLGB.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_Taxid=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1503-4R;
RA MEDLINE=92079888; PubMed=1745226;
RX Kiel J.A.R.W., Boels J.M., Beidman G., Venema G.;
RT "Molecular cloning and nucleotide sequence of the glycogen branching
RT enzyme gene (glgB) from Bacillus stearothermophilus and expression in
RT Escherichia coli and Bacillus subtilis.";
RL Mol. Genet. 230:136-144(1991).
CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF
CC GLYCOGEN.
CC -1- PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.
CC -1- MISCELLANEOUS: THE TEMPERATURE FOR OPTIMAL ACTIVITY IS
CC APPROXIMATELY 55 DEGREES CELSIUS.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb.sib.ch)
CC -----
DR EMBL_M35089; AAA22482.1; -.
DR PIR_S18599; S18599.
DR InterPro: IPR000461; -.
DR Pfam: PF00128; alpha-amylase; 1.
KM glycogen biosynthesis; Transferase; glycosyltransferase.
FT ACT_SITE 309 309 BY SIMILARITY.
FT ACT_SITE 352 352 BY SIMILARITY.
FT ACT_SITE 420 420 BY SIMILARITY.
FT ACT_SITE 420 420 BY SIMILARITY.
SQ SEQUENCE 639 AA; 74795 MW; F5BD4446B371E03A CRC64;

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Query Match 12.6%; Score 572; DB 1; Length 639;
Best Local Similarity 26.0%; Pred. No. 6,1e-34;
Matches 184; Conservative 109; Mismatches 232; Indels 182; Gaps 28;

QY 177 YEGSLDPSKQYKFGF---SRSETGITYREMAPGATWALIGDENNMN--PAADYTON 231
DB 15 HEGSL---YKSYELFGAHVLIKKNGMVGTRFCVAPARAREVLGSEFMENGTENMLKYS 71
QY 232 ECGWELEFLPNADGSPRIHGSVKIRMDTPSGN--KDSIP-----AMIKFSV 278
DB 72 NQGVMMIFIPENLE-----GLIKYTEITTDGNNVLKSDPYAFYSELPRHASYINI 124
QY 279 QAPGELPYNGIYYDPPREKQYVFNKPPKSLRIYESHVG--MSSTEPVITYANFRD 336
DB 125 KG---YQMNQGTMRKKORRRIYDP-----LFYELHFGSMKKKEDOSFTYQEMAE 174
QY 337 DVLEPRIKLYNAVOLMAIDESHYASFGYHVTNFAASSRFGTPDDLSLIDKANEGL 396
DB 175 ELIYVLEHGFTHIELDPLVEHPEDRSMGYOGIGYASATSRGYTPHDLMFIDRCHQAGI 234
QY 397 LYLMDIYHSHASTITLDGLNMFQSTDGHYHSGPRGHHMMMSDRLETVSGWEVLRELSN 456
DB 235 GVILDMWPGHFCCKDS--HGLYFEDGAPAYETANMODRENYWGTANFDLGPVRSFLISN 293
QY 457 ARWMLDEKFPDGFEDGVTSMYTHHGLQVDTGNVNEYGYATDVAVVYLMILNDMIH 516
DB 294 ALFMEYFPHVDGFRVDVANMLYFNS--DVLKRYTY-----AVFELQKINETVF 341
QY 517 GLPFEAVTIGEDVSGMPTVCIPVEDGGVGFDRYLHMAVADKWEIIOKREDEMKDIYH 576
DB 342 AYDNPILMIADSDTMDPRVAPFYDGLGIFNYK-----NNMGMMND 382
QY 577 MLT-----NRWLEKCY-----SYAE-----SHDQALVGDKTIATFWMADKMDTDFM 617
DB 383 ILTYETPPERHKKVHNKVFSLIYAVSENFILPFSHDEYVHGKSL----- 429
QY 618 ALDRSTPLIDRGVALHKM-----IRLITMGLGGEY-----LNFMGNEFGH 659
DB 430 -----LSKMPQTYEERFQJRL-----XYLLTHRGKLLTMGSGFQG 468
QY 660 -PEWIDFPRGDLHLPSEKFPVGNNSYDKCRRPDLGNSKHL-----RYHGQEF 708
DB 469 FDEKMDLEQDMLM-----FD-----FDMRNMMYVKELLYCKYKRYKPYLXL 511
QY 709 DQAIQHLF--EAYGFMTSEHGYISRKDERDLIYFEGNLVYFNFMTSSYSYDIRGCL 766
DB 512 DHPDGEFEMIDVHNAEQSIFSIRGRKEDDL-----LIVCNF--TNKVYHGYKVGVP 563
QY 767 KPGYKVIYLDSDPLFGGFGRLSHDAEHFSPGWDNRPSFMVYTP 813
DB 564 LFTIRREVINSDAIQFGFGNI--NPKRIAMEGPFHGRKPHIQWTIP 609

RESULT 9
GLGB_ECOLI STANDARD: PRT: 728 AA.
ID GLGB_ECOLI STANDARD: PRT: 728 AA.
AC P07762;
DR 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE 1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOGEN BRANCHING
ENZYME).
GN GLGB.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=86250792; PubMed=3013861;
RA Baecker P.A., Greenberg E., Preiss J.;

```

RT RT "Biosynthesis of bacterial glycochen. Primary structure of Escherichia coli 1,4-alpha-D-glucan:1,4-alpha-D-glucan 6-alpha-D-(1,4-alpha-D-glucano)-transferase as deduced from the nucleotide sequence of the glg B gene." J Biol. Chem. 261:8738-8743(1986).

RL [2]

RA RA SEQUENCE FROM N.A.

RA RA STRAIN-K12 / MG1655.

RA RA MEDLINE-97426617; PubMed-9278503.

RA RA RILEY M., F.R., BLUMFELD G. III, BLOCH C.A., PERNA N.T., BURLAND V., GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J., MAU B., SHAO Y.

RT "The complete genome sequence of Escherichia coli K-12." Science 277:1453-1474(1997).

CC -1 CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF GLYCOGEN.

CC -1 PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.

CC -1 SUBUNIT: MONOMER.

CC -1 SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.

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CC EMBL: M13751; AAA23872.1; -

DR EMBL: U18997; AAA58230.1; -

DR EMBL: AE000419; AAC76457.1; -

DR PIR: A25498; NOCCA.

DR EcGene: EG10378; glgB.

DR InterPro: IPR000463; -

DR Pfam: PF00128; alpha-amylase: 1

KW Glycochen biosynthesis; Transferase; Glycosyltransferase.

FT ACT\_SITE 405 458 BY SIMILARITY.

FT ACT\_SITE 458 458 BY SIMILARITY.

FT ACT\_SITE 526 520 BY SIMILARITY.

FT SEQUENCE 728 AA; 84536 MW; 0F20AF3677BF2015 CRC64;

Query Match 12.6%; Score 571.5; DB 1; Length 728;  
Best Local Similarity 25.4%; Pred. No. 6.1e-34;  
Matches 205; Conservative 110; Mismatches 276; Indels 217; Gaps 32;

QY 105 MDDKIVDEVNK-----ESVPMRETVSIRKIGSKPRSTIP-----PGRGQ 145  
DB 1 MSDRIDRIVINALAGHAFDFSVYGMHKTAA---GLEVALLPDADVAVIEKTRK 56  
QY 146 IYDID-PSLTGF-----RQHLIDYRS-----QYKRAREIDKYEGLD 182  
DB 57 LAKIECLDSRSEFFSGVIRRRKNFEYQOLAVVHGOQNLIDDPYRFGPLIOEDMWLSEG 116  
QY 183 AFSRQYEKFGESRSE---TGITYREMAFGATWALIDDPNNMNPNAVM--TQNECGVE 237  
DB 117 THLRREYELGHAADMDVDTGTREVSVMAPNARVSVVGQVPMDDRHRPMRLRESGIWE 176  
QY 238 IFLPNNADGSPPIPGSHVKIRMPDPSGNKDSIPAMIKFSVOAPE-----LPYNGIT 290  
DB 177 LFIEG-----AHNGQLKYEMIDANONLNLKSDPAFEADQMRETSLLCGLEPKV- 228  
QY 291 YDPPEEKVEYKKNQPKPKSLRTYESHVGSSTPEVINYTYANR---DDVLPRIKRIKY 347  
DB 229 -QTEERKKAQDFAP-----ISTIEYHGLSWRRITDNFNLISRELADQILPAKMGF 281  
QY 348 NAVOLMAIQEHSYASRGYHVTNFTYAASSRFGTPDLKSLIDKAHEGLLVMDIVSHA 407  
DB 282 THLELQPLINERDFGSSWQYPTGLYAPLRRRGTRDREYFIDAAHAAGLVILMWPDHF 341  
QY 408 STNTLIDGNMFDTGDGHYHSGPR-GHHMMWDSRLFNYSGWSEVLRFLLSNARWMLDEYK 466

Df 342 PTDFE -ALAEFGDTN -LYEHSDPRRGYHQDMWTLTYNGREAVENFLVGNALTYMIDREFGI 399

Oy 467 DGFPEQSVTSMATHTHSGLOVDFTGWNINFEY-----PGUADVAUVUULLLMDMIHGILFPEA 522

Dd 400 DALRYADVAMSTR-----DYSKREGEMIRPERGGRENLEAFGLANTNRILGEIAYSGA 453

Oy 523 VTIGEDVSCGPYICLYEECGVGFDURLHMAVADKWITIIOKREDMKMGDIYHMINTNR 582

Dd 454 VTMKEESTDPGVSRPQDMGSLGWFK-----NWLG----- 484

Oy 583 WLEKCVSYAE-----SHDAQLVGDKTIAFLMDIKOM 613

Dd 485 WMHDPTLDYMLDEIVYROYHNDRKLTEGLLYNTENTVPLRLSHDEVVHNGKI----- 535

Oy 614 YDFMALDRPSTPLRIDGVALFMKIMILTMGLGEGSY-----LNMGNEFCH-PE 661

Dd 536 -----LDRMF-----GDAMOKFANL-----RAYUGMMVAFFPKRLRLPMGNEPIAGSE 577

Oy 662 WIDEPRDDLLPGRKFVPNNNSYCKRRRDLGSKRLRYHGOEPDAOIHLAEIAYGF 721

Dd 578 WMNDASLDWMTLBGS-----GDMNHGYOURLVRL-NLTFRHHKAHEID-----FDPPG 626

Oy 722 MTSHOVISKIDRKDIIVFEER-----GNLYEVENNHNMTSSDYRVASCLEPKYGK-VLOS 777

Dd 627 -----EWLVYDDKERBVLIFVRDKEGNEIIIVASNFYPRPHDVFQINGMRRIILWT 681

Oy 778 DDPLFGFGFR-----LSHOAH 794

Dd 682 DSMHYGSNANGNGVYHSDEITASGRQH 709

RESULT 10

AC GLGB\_HAEIN STANDARD; PRT; 730 AA.

ID ID GLGB\_HAEIN STANDARD; PRT; 730 AA.

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE 1.4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOCEN BRANCHING ENZYME)

GN GLGB OR H11357.

OS Haemophilus influenzae.

OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;

CC Haemophilus.

OX NCBI\_TaxID=727;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-RD / KW20 / ATCC 51907.

RX MEDLINE=95350630; PubMed=7542800;

RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirtaneis E.F., Kerlavan A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.H., Scott J.D., Shirley R., Liu L.-I., Glodak A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton H.D., Wetterback T.R., Hanna M.C., Nguyen D.T., Saubko D.M., Brandon R.C., Raehne L.D., Frichman J.L., Fuhmann J.L., Georgagen N.S.M., Frazer C.M., Smith H.O., Venter J.C.;

RA "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";

RT Science 269:496-512(1995).

RL -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCCSIDIC LINKAGES OF GLYCOCEN.

CC -1- PATHWAY: THIRD STEP IN GLYCOCEN BIOSYNTHESIS.

CC -1- SUBUNIT: MONOMER (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.

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EMBL: U32815; AAC3004.1; -  
DR TIGR: H11357; -  
DR InterPro: IPR000461; -  
DR Pfam: PF00128; alpha-amyase; 1.  
KW Glycogen biosynthesis; transferase; Glycosyltransferase.  
FT ACT\_SITE 405 405 BY SIMILARITY.  
FT ACT\_SITE 458 458 BY SIMILARITY.  
FT ACT\_SITE 526 526 BY SIMILARITY.  
SQ SEQUENCE 730 AA; 83820 MW; 5B9575317P53/69A CRC64;

Query Match 12.5%; Score 566; DB 1; Length 730;  
Best Local Similarity 24.9%; Pred. No. 2e-33; Indels 196; Gaps 38;  
Matches 209; Conservative 139; Mismatches 295;

61 MYASKRVLDPGRICYSSTDLAAGTVSESOVLTVESLIMDK--IVEDEVNKE 117  
1 MTTAVVQALIDGFPD--ASNGDPFALGMETEGGT--ELRTLLPANRVVIERESGKE 56  
118 SVPMRETVSIRK--IGSKPRSIIPPGRGORITIDPSLIGFRHLDYRSQYRLKEID 175  
57 ITTEL-DCVDERGFEVVG--VIPNCKOPFAYOLOVFWGNEAOIIPDY-RFHPMIDDLE 109  
176 KYGSSLDASFGRYKKEGFSNSE--TGIRBMAPCATMAALIGFNMNPNADVMT-Q 230  
110 QWLISGSMRLRPEVLAHMECDGVGVNFRMLAPARAVSYIGDPTWDGRHPRH 169  
231 NECGWEIFLPNNADG--SPPIHGSRYKIRNDTPSGNKDSIPAW 273  
170 SKGSWMLFLPKASLGQLYKFLIDCHGNLRKADPPAFSS--QLRDTAS-QVSLAPNV 226  
274 IKESVQAPGELPYNGIYDPPPEEKVYFKPQPKRPSLRITSHVGMSTEVYIN--T 330  
227 VEMT--EARKKANOONP--ISIEYHVLGSMRNLNNEMWLD 264  
331 YANRDOVLRIRIKLGNAYVOLAIOHSHYAVTFVYAASSFGPDDLKSLIDK 390  
265 YDQADLDELIVYKEMGTHTLEPLSEPPDGSWGTOPDLYSTSRFSGPEFRRLVKR 324  
391 AHEGLILVMDIYHSHASTVTLGLNMFDSGDHYHSGPR-GHHMMWDSRLPNYGSWEY 449  
325 AHEGLIVILMDVWGHPRSPDT-HGLVAFDGT-ALYEHEDPREGHQWMTLIVYNGNEV 382  
450 LRFILSNARWLDYKFKDGRFRFGVYSMTTHGLQVDFGNNEY--FGATIDVAY 505  
383 KNFLSSNALYWLERFGVDGIRVAVASMIYR--DYSRABGEWIPNOYGGRENLEAI 436  
506 VYIALLMDMIHGLPEAVTIGEDVSGMPVPCIPVEDGVGFDRHLHAAVADKWEIIQKR 565  
437 EFLKHTMKIKHSEMAKALISTAEESTFAGYTHPSENGLGIFNKRMMNG----- 464  
566 DEDWKMDIYHMLT--NRRLKCVSYAE--SHDQ--ALVGDXTI 604  
485 --MMNDTLAVMKIDPIYRQYHNKMTFGMYQSENFVPLSLHDEVLHGKYSILKMPG 541  
605 AFWLMDDM--YDFMALDRSTPLIDRGVALHMKILITMGGLGEGEYLPMFGNREGH-P 660  
542 DTWOKFANLRAVYGYM--WGIPGKLL-FMGNEFQGR 576  
661 EM--IDPRGLHPSG--KFVPGNNYSYDKCRFRPDLGNSKHLRYHGMQEPD 709  
577 EMNTEESIDWLDLIDENIGGHHKVLKLVKDNOIYQKNRPLFELDSSPE----- 626  
710 QAIOHLEAVGEMTSEHOYISRKDERDRIIVERGN--LVEFVNFHTSSTSYDRVG 764  
627 --GF--DMLVDDAANSVLAFFERRSNGERIIYVSNFTVPRH-NYRIG 670  
765 CLKRGKTIYVDSDDLPL--GGFRLSHDAHFSEGVNDKRRPSFWYVPCRRVAV 819

DB 671 VNAVAKYEELIINTDSMYEGSNVGNFGVA--SEQIESH-----RENSISVIP-PLATV 723  
QY 820 Y 820  
DB 724 Y 724

RESULT 11  
ID GLGB\_AGRU STANDARD; PRT; 734 AA.  
AC P52979;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE 1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOGEN BRANCHING ENZYME).  
GN GLGB.  
OS Agrobacterium tumefaciens.  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Rhizobiaceae; Agrobacterium.  
OX NCBI\_TaxID=362;  
RP SEQUENCE FROM N.A.  
RC STRAIN=A348;  
RX MEDLINE=99069330; PubMed=9851999;  
RA Ugalde J.E., Lepek V., Uttaro A.D., Estrella J., Iglesias A.,  
RA Ugalde R.A.;  
RT "Gene organization and transcription analysis of the Agrobacterium tumefaciens glycoen (g1g) operon: two transcripts for the single phosphoglucomutase gene."  
RT J. Bacteriol. 180:6557-6564 (1998).  
RL -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF GLYCOGEN.  
CC -1- PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.  
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOYL HYDROLASES. ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.  
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CC DR EMBL: AF03856; AAD03472.1; -  
DR InterPro: IPR000461; -  
DR Pfam: PF00128; alpha-amyase; 1.  
KW Glycogen biosynthesis; transferase; Glycosyltransferase.  
FT ACT\_SITE 417 417 BY SIMILARITY.  
FT ACT\_SITE 470 470 BY SIMILARITY.  
FT ACT\_SITE 538 538 BY SIMILARITY.  
SQ SEQUENCE 734 AA; 83623 MW; 70A3CD35A77F31E6 CRC64;

Query Match 11.9%; Score 542.5; DB 1; Length 734;  
Best Local Similarity 23.8%; Pred. No. 1e-31;  
Matches 182; Conservative 123; Mismatches 266; Indels 193; Gaps 32;

119 VPMRETVSIRKIGSKPRSIIPPGRGORITIDPSLIG-----FRQHLDYRSQ-- 166  
36 IPLHETPE--GFSARCFIPGAEEVSVLTGONFVGLKQIDPPGFFGRIDLSKRQPV 91  
167 YKRLREE-----IDKY--EGSLDAFSRGYKFGFS-RSETGITRE 204  
92 RYRACDDADENAVTDPYSFGLVGPMDVYFREGSICGSTGMARPLKLEGVDFHFAV 151  
QY 205 WADGATMAALIGDENWNPADVMT-QNECGWEIFLPN-----NADGS-PPL- 250  
DB 152 WAPNGRRVSVYGVFNWMDRRHMYRFRKDTGIMEIFADPVYACAYKFFELGANGELPLK 211  
QY 251 --PHGSRVAKIRNDTPSGNKDSIPAWIKFSVQAPGELPYNGIYDPPPEEKVYFKPQPKR 308

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D 212 ADPARRRELAPKNA-----SYTAP-ELTOK-WEOAIRREHA---QVDR 252
O 309 PKSLRYESHG--MSSEPIYNTYANFRDVIYPRIKKLGYNVQMAIOESHYSFQY 366
D 253 RQPSITIEVHAGSMORSDGDFLSDLEAOLITCTDGMGTHTEHPTIEHPIDPSWG 312
O 367 HTVTFYAASSFFTPDDLSLIDKAHELGLVLMIDYHSHASTVTLGLNMFDTGCHYF 426
D 313 OTTGATATARDEGDEGPARFVNGAKVGGVGLDWPAPHPDE-HGLWFOET-ALYE 370
O 427 HSGFR-GHHMMWDSRLFNYSQWELREFLSNARWMLDEYKDFGFRDGYTSMVYTHGLQ 485
D 371 HADPRGHPDMNTAIXNFGRIEVMSYLNNALYMAERFHLGLRVAVASMLY----- 424
O 486 VDEFTGNNEY---FGYATDVAVVYLMMLNDMIGLFEPAVITIGEDVSGMPTVCIPEV 541
D 425 LDYRKRGEWYIPNEYGGRENLESYVFLQKNMSLYVGTGPMVTAIBESTWPKYQFVHE 484
O 542 GGVEFDYRLHMAVADKWEIIOKRDEDMKG-----DIVHMLTNRRLKCVSY 590
D 485 GGLGFGFK-----WNMGFMHDLTSYFSPREYHRRKPHHOELTEGLY 525
O 591 A-----ESHDOALVGDKTIAFWLMDKMDYDMALDRSTPLIDRGVALHMKIRLITM 642
D 526 AFTEFNFLPSHDEYVHGKSLIDKAKSGDDMOKEANL-----RSYGFPM 570
O 643 GLGEGYLNFGNEFGH-PEWIDFPRGDLHLPSGKFVPGNNYSYDKORRFDLGNKHLR 701
D 571 GYPRKTL-FMGQFPAQMSMSE--KQSL-----DMNLR 601
O 702 YHMGCE-FDOALQLEAAGFPMSEHOYISRKDERDRIYFERGNLVEYFNFM----- 754
D 602 QYPRHEGRKRLVRLNLTYSKALHARDEPDRFWLVVDHNSVFA---WLRTAPG 657
O 755 -----TSSY-SDRYGCLAPKRYKYVLDSDPFLGFGFR 787
D 658 EKPVAVYICNLTPYRENYVPLVAGRWRLMTDAETIGSGK 701

RESULT 12
GLGB_BACCL STANDARD; PRT; 666 AA.
AC P30537;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOGEN BRANCHING ENZYME).
GN GLGB.
OS Bacillus caldolyticus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93208370; PubMed=1296817;
RA Kriel J.A.K.W., Boels J.W., Belman G., Venema G.;
RT "The glbB gene from the thermophile Bacillus caldolyticus encodes a
RT thermolabile branching enzyme.";
RL DNA Seq. 3:221-232(1992).
CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF
CC GLYCOGEN.
CC -1- PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.
CC -1- MISCELLANEOUS: OPTIMAL ACTIVITY AT APPROXIMATELY 39 DEGREES
CC CELSIUS.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z14057; CAA78440.1; -.
DR InterPro: IPR000461; -.
KW Pfam: PF00128; alpha-amyase; 1.
KW Glycogen biosynthesis; transferase; Glycosyltransferase.
FT ACT_SITE 309 309 BY SIMILARITY.
FT ACT_SITE 352 352 BY SIMILARITY.
FT ACT_SITE 420 420 BY SIMILARITY.
SQ SEQUENCE 666 AA; 166431495BBI6E CRC64;

Query Match 11.9%; Score 539.5; DB 1; Length 666;
Best Local Similarity 26.9%; Pred. No. 1.5e-31;
Matches 181; Conservative 93; Mismatches 238; Indels 161; Gaps 26;

O 177 YEGSLDAFSGYKFGF-----SRSETGITYREMAPGATMAALIGDFNMN--PNADVTQN 231
D 15 HEGRL---YQSEYELGAYIRGGAAGVTRFCVMAHAEVRLVGSFNMGNTNSPLTKVN 71
O 232 ECGWEIPLPNNAQS---PIPHGSRYKIMDPPSGNKSIPAWIKFSVQAGELPYN 287
D 72 DSGVWTIVYRNLKHLKYLITPDGKYLKADYAYSELPHITASIVYDLKG-YENN 130
O 288 GIYDPREREKTVFKNPQPKRKSRLRYESHVGMSTEP--VINTYANFRDVIYPRKYL 345
D 131 DSPWOKKKRKRKLTDP-----WITELHNGSKKKRPGFRFYIRMADELIPYLER 183
O 346 GYNVQMAIOESHYSYASGCHVNTFYAASSRFPDDLSLIDKAHELGLVLMIDYHS 405
D 184 GFTHLELPVLEHPLDRSMGYOGTGYSTYSKYGRPHCFMVFDCHQAGLVIIDWPG 243
O 406 HASTVTLQNLNFDGTDGHYFHSRGRHMMWDSRLFNYSQWELREFLSNARWMLDEYK 465
D 244 HFCKDA-HELTYMFGDAPYEVANENKDRRENYWGTANFDLGRPEVNSFLISNALFWLEYH 302
O 466 PDGFRFDGVTSMYTHNGLQVDFGTNENYFGYADVAVVYLMMLNDMIGLFEPAVTI 525
D 303 YDGFVDAVANLWPNNDRL---YENPY-----AVEFLQNLNVAAYVPMWMI 350
O 526 GEDVSGMPTVCIPVEDGVDGYRLHMAVADKWEIIOKRDEDMKGDIYVMTL----- 579
D 351 ABDSTDMPRVTAPTYDGGIGFNK-----NMGGMNDMLKYETPRP 391
O 580 -RRRLKCVS-----YAE-----SHDOALVGDKTIAFWLMDKMDYDFVALDRPSTPL 626
D 392 HERKTAHNGVPSLLYVASENFIPLFSHDEYVHGKSL----- 429
O 627 IDRGVALHKM-----IRLITMGAGEGY-----LNMGNFEGH-PEW----- 662
D 430 -----LNKMGOSYIEKRAQLRL-----YGYMAHNGKLLRWGSEFAQDFDRAE 477
O 663 -----IDPRGDLHLPSGKYVPGNNYSYDKCRRRDLGNSKHLRYHGMQFDOAIHLEE 717
D 478 LDWVLEDF---ELHRKMEYVKOLIACTKRYKPYELD-----HDPREGWIDVINA 527
O 718 AYGMTSEHOYISR-KDERDRIYFERGNLVEYFNFMSTSSYDRYGCLKPKKYI;TLD 776
D 528 -----QSIFSEIRKKGKGD-----VLIVCNF--TNOAYDYKVSVPDLAPYIEVLN 573
O 777 SDDPLFGGFRLS 789
D 574 SDAAEFGSGSHVN 586

RESULT 13
GLGB_BUTFI STANDARD; PRT; 639 AA.
ID GLGB_BUTFI
AC P30539;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)

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FT ACT SITE 464 464 BY SIMILARITY  
FT ACT SITE 532 532 BY SIMILARITY  
SQ SEQUENCE 731 AA: 81729 MW: EE2BEF765352617 CRC64:

Query Match 11.58; Score 524.5; DB 1; Length 731;  
Best Local Similarity 24.78; Pred. No. 2,1e-30;  
Matches 187; Conservative 119; Mismatches 258; Indels 193; Gaps 32;

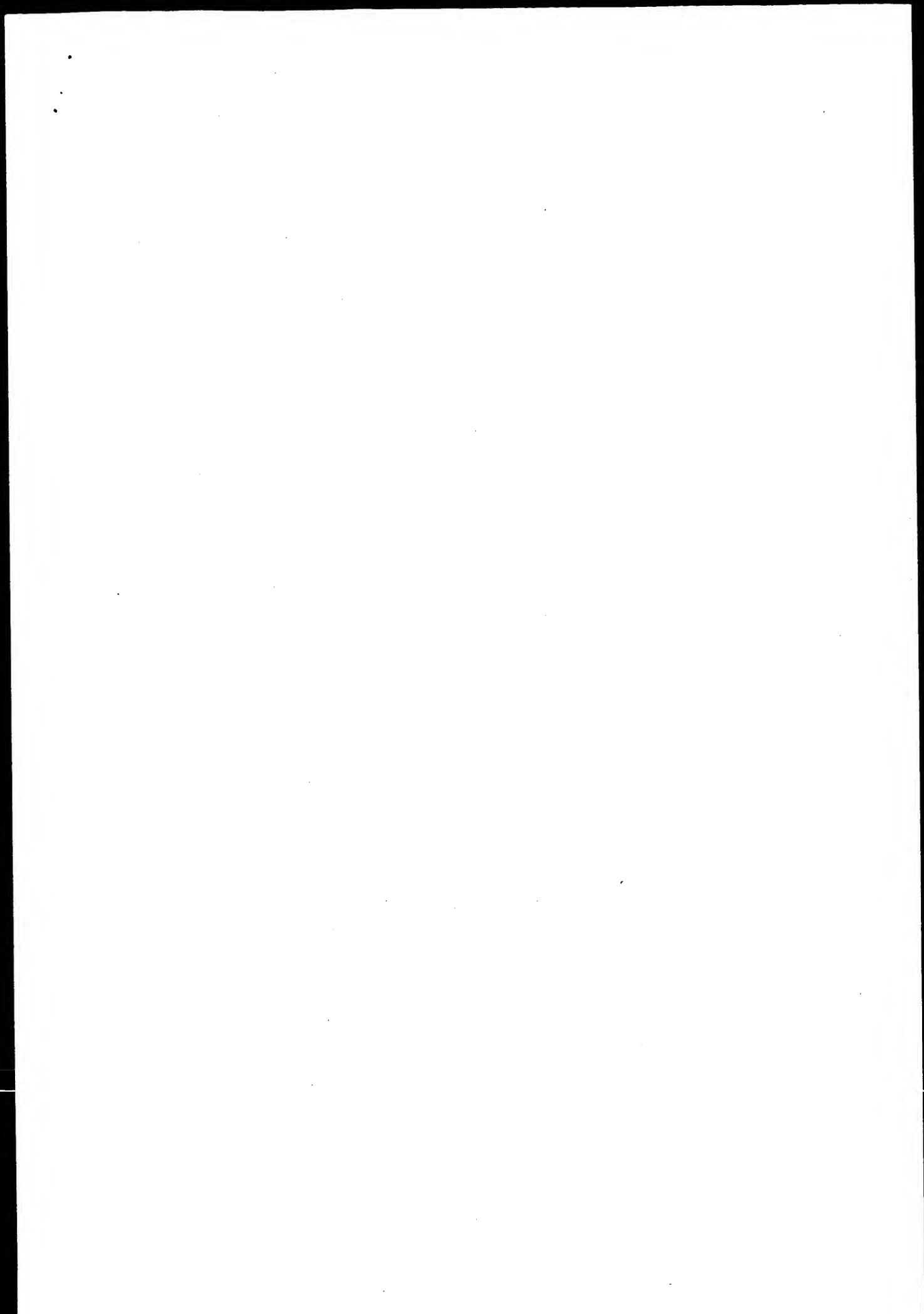
Db 131 GSKPRIPPGCORIYDIDSLTGLFRQHLDRYSQYKRLREEDIKYEGSLDAFSRGEK 190  
Db 94 GCEPHTVAD-----AYRFLPLTGLVVDLHL-FAEGRHRELTWEVGAHPRS----- 136  
Db 191 FGFSRSE---TGITYREMAPGATMAALIGDFNNMNP-ADVMTONEGWEIPLP----- 241  
Db 137 -FTTADGVGVSPFAVAPNAKGVSLIGEPNGNNGHAPRYLGPBGWELFWPDPD 194  
Db 242 -----NNAGD-----SPRLPHGSRYKIRMDTFSGNKDSIPAMIKFSYVAPGELPYNGI 289  
Db 195 GLYKRVYAGADGVYDRAADPAFGEVP--PQTASRYTSSTYTWGDDMMAGRLL----- 247  
Db 290 YYDPPEEKYVFKRQPKRPSLRKRYESHVMSSTEPYINTYANFRDYLPRIKKLYNA 349  
Db 248 -----RNFV---NEAMSTYVHLG--SWRPEL-SYROLARELTDYIDVQGFTH 289  
Db 350 VOLMAIQESHYASFGYVNTFYAASSRFGTPDDIKSLDKRAHELGLLVLMYVSHAST 409  
Db 230 VELLVAHPRPAGSWGIVYVAPTSTFRGTPDPRALVDALHOAGIGVYDVPVAFHPK 349  
Db 410 NTLGLNFDGTGDIHYEHSR-GRHHMMWDSRLNYSWEVLEFLLSNARWMLDEYKEDG 468  
Db 350 DAM-ALGRFFDTP-LYEHSDPKRGEOIDMGTYVDFPGRVEYRNLVANALYLOEFDHIG 407  
Db 469 FRFDGVTSMYTHHGL-QVDFGNYNEFYGATVDAAVYLMMLNDMIHGLPREAVTIGE 527  
Db 408 LRVAVASMLTLDYSRPGCVTPVNH--GGRENLEAVQFOENKNAFAHKAFCIVTIAE 464  
Db 528 DVSGPRTYCIYEDGVGFEDRYLMAVADKWEITOKRDEDMKMGDIYVHMLNTRMEK 587  
Db 465 ESTPMSGVTTRTNIGLGFSMK-----MNNG-----WMHDT 495  
Db 568 VSYAE-----SHOALVGDITAFMLDKMYDPM 618  
Db 496 LDVSRDVTYSYHHNHTFMSLYAFSENIVYLPISHDEVHGKTL--WGR----- 544  
Db 619 LDRSTPLIDRGVALHMKIRLITMGLOGEGYLANMGNEFG-HPRW-----IDPRGDLHL 672  
Db 545 --MGNNHV-RAAGLRSLAYQMAHPGKO--LTFMGQGFGRAMWSORGLDMFQDLD-- 596  
Db 673 PSGRFVPGNNYSYDKCRRRFDLGNKHLRHGMOEQDOALQHLLEAVGFMTS-----EH 726  
Db 597 -----ENGFS-----NGIQLRVADIDIDYRCHPALMSLDTTPEGY 631  
Db 727 QYISKRDERRIIVEER-----GNLVEVFNFHMTSSYDYKVGCLKPGKYIVLSDPDL 781  
Db 632 SWIANSANNVLSFMRGSDGLVACVFNEA-CAEHRDYLDLPRAGRRREVLTADATI 690  
Db 782 FGCGRLSHDAEHFSFEGWYNDRRSEFVYTPCRTAV 818  
Db 691 YHSGIGNLGVDATDPMH-GRPASAVLVLPPTSAL 726

RESULT 15  
GLGB\_BACSU STANDARD; PRT: 627 AA.  
ID GLGB\_BACSU  
AC P39116:  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE 1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOSYL BRANCHING ENZYME).  
OS GLGB.  
GN  
Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Bacillus.  
OX NCBI\_TaxID=1423;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=168;  
RX MEDLINE=94195107; PubMed=8145641;  
RA Kiel J.A.K.W., Boels J.M., Belman G., Venema G.;  
RT "Glycogen in Bacillus subtilis: molecular characterization of an operon encoding enzymes involved in glycogen biosynthesis and degradation.";  
RL Mol. Microbiol. 11:203-218(1994).  
RN (2)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98048467; PubMed=9387221;  
RA Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;  
RT "Sequencing and functional annotation of the Bacillus subtilis genes in the 200 kb rmb-dnaB region.";  
RL Microbiology 143:3431-3441(1997).  
CC -1- FUNCTION: CATALYZES THE FORMATION OF THE ALPHA-1,6-GLUCOSIDIC LINKAGES IN GLYCOGEN BY SCISSION OF A 1,4-GLUCAN CHAINS AND THE SUBSEQUENT TRANSFER OF THE OLIGOSACCHARIDE TO OTHER PARTS OF ALPHA-1,4-GLUCAN CHAINS.  
CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF GLYCOGEN.  
CC -1- PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.  
CC -1- INDUCTION: EXPRESSED EXCLUSIVELY ON MEDIA CONTAINING CARBON SOURCES THAT ALLOWED EFFICIENT SPOULATION.  
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.  
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CC  
CC  
CC EMBL: Z25795; CAAB1040.1;  
CC EMBL: AF008220; AAC00214.1;  
CC EMBL: Z89119; CAB15076.1;  
CC PIR: S36624; S36624.  
CC Subtilisin; B610907; 9198.  
CC InterPro: IP000461;  
CC Pfam: PF00128; alpha-amyase; 1.  
CC Glycogen biosynthesis; transferase; glycosyltransferase.  
CC ACT\_SITE 309 309 BY SIMILARITY.  
CC ACT\_SITE 352 352 BY SIMILARITY.  
CC FT 420 420  
CC SEQUENCE 627 AA: 73665 MW: 64B0A553B6767BA CRC64;  
SQ  
Query Match 11.4%; Score 518.5; DB 1; Length 627;  
Best Local Similarity 26.9%; Pred. No. 4.6e-30;  
Matches 175; Conservative 106; Mismatches 254; Indels 115; Gaps 24;  
Db 177 YEESLDAFSGKGEYGFSSSE---TGITYREMAPGATMAALIGDFNNMNPADVMTQ-N 231  
Db 15 HEGSSL--FKSYQLRSHRELNGSKGYEFCVMAHASEVRAVAGDFNMSGGEHYVHRVN 71  
Db 232 ECGVWEIPLNNADSGSPRLPHGSRYKIRMDTPSGN-KDSIPAMIKFSVOAP--GELPYNG 288  
Db 72 DNGIWTLPFG-----IGEKERYKELYVNNGELRLKADYALYSEVRPTASITDLD 124  
Db 289 IYDPPEEKYVFKRQPKRPSLRKRYESHVNG--MSSTEPYINTYANFRDYLPRKKG 346  
Db 125 EGSWMDQWOKRQAKLTLYEPVLYELHLGSKHSDGRYSKELSGTLPIPKKHG 184  
Db 347 YNAVOLMAIQESHYASFGYVNTFYAASSRFGTPDDIKSLDKRAHELGLLVLMYVSH 406  
Db 185 FTHIELLPYEHPRDPSRWGVOCTGYSPTSRPGPHDLMKFVDECHOONIGVILDMVPGH 244

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OY 407 ASTNTLDGLMFDGTGHTFHSGPRGHMMDSRLFNYSWEVLRFLLSNARWMLDEYKF 466
Db 245 FCKDA-HGLYMFDEGLPEYKEERDRRENNMLMGTFANFDLGRPEVHSFLISNALYWAEEFYHI 303
OY 467 DGRFDGVTSMYTHHGLQVDFGTGNYNEFGYATDVDAVYVYMLLNDMIGHLFPEAVTIG 526
Db 304 DGRFDVAVANILY-----WPNODERH---TNPYAVDFLKLNOYMRREAYPHVMIA 351
OY 527 EDVSGMPTVCIPYEDGSGVGFYRLHMAVADKWVEIIQKRDWDWKGDIIVHL---TNR 582
Db 352 EDSTEMPQVYTGAVEEGGLGFHYKMMG-----W-MNDVLYKMETPEERR 395
OY 583 WLEKCVSYA-----ESHDAVGDKTIAFWLMDK---DWTDFMALDRPSTPLI 627
Db 396 HCHQLISFSLYAFSEHFVLPFSHDEYVYKKS---LTKMPGDYWKFAQYR---LL 447
OY 628 DRGVALHKMIRLITMGLGGEGYLNFMGNERGH-PEMIDFPRGD-----LHLPSCKEVP 679
Db 448 LGYMTYHPGKLLI-----FMGSEFAQFDEMDTEQLDWFLDSFPMHOKASVFTQ 496
OY 680 GNNYSYDKCRRRPDLGNSKHLRYHGMQEPDOAIQHLLEAYGFMTSEHQYISRKDERDRII 739
Db 497 DLLRFYQKSKILIY-----HDHRAQSFEMIDVHNDEQSI--SFIRYQKKGHA---- 543
OY 740 VFERGNLVEFENHMTSSYSQYRVGCLKPGKYIVLDSDDLFGGGRLS 789
Db 544 -----LVYICNF-TPVYVHQYDVGVPFTQYLEVLSNDSSEYGGSGGIN 586
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Search completed: August 7, 2001, 11:20:44  
Job time: 141 sec



Accession	Host	Isolate	Strain	Genotype	Phenotype	Pathogenicity	Notes
33	161	3.5	549	1	AGLA_RHIME		Q923r8 rhizobium m

FT	58	799	1,4-H
CHAIN			

ACT_SITE	394	394	1,4-ALPHA-GLOCAN BRANCHING ENZYME 11B. BY SIMILARITY.
ACT_SITE	394	394	1,4-ALPHA-GLOCAN BRANCHING ENZYME 11B. BY SIMILARITY.

FT ACT\_SITE 447 447 BY SIMILARITY.  
 ACT\_SITE 516 516 BY SIMILARITY.  
 SO SEQUENCE 799 AA; 90517 MW; 0B440E03778B087A CRC64;

Query Match 69.5%: Score 3160; DB 1; Length 799;  
 Best Local Similarity 70.3%; Pred. No. 5.2e-222;  
 Matches 583; Conservative 83; Mismatches 95; Indels 68; Gaps 8;

2 GHYTSIGIRPCAPLCKSQSGFHCYRTSSCLSPNFEEAFSRVFGSKSSHEDSSVM 61  
 33 GLETLRGARVGC-----SGTHAMRAA-----AAARKA-----YM 62  
 62 VYASKRVLPDC---RIEYSSSTDLLEAPGVSESOY---LTVESLIMDKIVEDEVN 115  
 63 YPEGN---DGLASRADSAQFOSDELEVP-DISELTGAGVADAQAL----- 106  
 116 KESVPMRETVSIRKIGSKPRSTIPPGRCQRIYDIPSTFGRHLDYRYSQYKRLREID 175  
 107 -----NRYRVPPSDOKIFQIDPMQGIKYLEYRSLKRLKSID 150  
 176 KYEGSIDAFSRGCEKFGESRSETGTYREMAPGATWALLIGDENMNPADVMTONEGCV 235  
 151 EHEGGLEAFSRSEYKFGFASAEITTYREMAPGAFSAALGVNMDPADKSKSNEGV 210  
 236 WEIIFLNNDGSPRIPIPGSRVAKIRMDTPSGNKSIPAMIKESVQAPDELPIYNGITDPE 295  
 211 WEIIFLNNDGSPRIPIPGSRVAKIRMDTPSGIKDSIPAMIKESVQAPDELPIYNGITDPE 270  
 296 EEKYVFNKPPKPKSLRIYESHVGSSTEPYINTYANRFDYDLPRIKKLGYNVQALMAI 355  
 271 EYKYVFNKPPKPKSLRIYESHVGSSTEPYINTYANRFDYDLPRIKKLGYNVQALMAI 330  
 356 QESHYSYAFGYHNTNYAASSRFGPDLDKSLDKAHELGILVMDIVHSHASTVLLDGL 415  
 331 QESHYSYAFGYHNTNYAASSRFGPDLDKSLDKAHELGILVMDIVHSHASTVLLDGL 390  
 416 NMEDGTDGHHFSGRGMHMMDSRLFNYSMEVFLRLSLNARWMLDEKFFGFRDGYT 475  
 391 NGEDGTDGHHFSGRGMHMMDSRLFNYSMEVFLRLSLNARWMLDEKFFGFRDGYT 450  
 476 SMATYTHHGLAVDTGNYNEFGATGVDVAVYMLNDMIGHFEPVAVIGEDVSGMPYV 535  
 451 SMATYTHHGLAVDTGNYNEFGATGVDVAVYMLNDMIGHFEPVAVIGEDVSGMPYV 510  
 536 CIEVEDGSGFEDYRLHMAVADKVEITOKRDEWKMGDIYHMLTNRMTLEKCVSAESH 595  
 511 ALPYHDDGVGFEDYRLHMAVADKVEITOKRDEWKMGDIYHMLTNRMTLEKCVSAESH 570  
 596 QALVGDKTIAFWLMDKMDYFMAALDRPSTPLIDRGVALHMKIRLITMGLAGEGYLNFGN 655  
 571 QALVGDKTIAFWLMDKMDYFMAALDRPSTPLIDRGVALHMKIRLITMGLAGEGYLNFGN 630  
 656 EFGHEWIDPPRGDLHLPSCGFYVGNNSYDKCRREDLGNKHLRYHGMQEFDAIOLH 715  
 631 EFGHEWIDPPRGDLHLPSCGFYVGNNSYDKCRREDLGNKHLRYHGMQEFDAIOLH 690  
 716 EEAQVGTSEHOYISRKDEDRILIVERGNLIVFNFHMTSYSDYRVGCLKGGKYIYL 775  
 691 EEAQVGTSEHOYISRKDEDRILIVERGNLIVFNFHMTSYSDYRVGCLKGGKYIYL 750  
 776 DSDPPLFGGFGRLSHDAHFSEFGWYNRPFSFVAVYPPCTAAVYALVE 824  
 751 DSDPPLFGGFGRLSHDAHFSEFGWYNRPFSFVAVYPPCTAAVYALVE 799

RESULT 2  
 ID GLGB\_SQUTU STANDARD; PRT; 861 AA.  
 AC P30924;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE 1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (STARCH BRANCHING  
 ENZYME) (O ENZYME).  
 GN SBE1 OR SBE.  
 OS Solanum tuberosum (potato).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; eusterids I;  
 OC Solanales; Solanaceae; Solanum.  
 OC NCBI\_Taxid=4113;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. DIANELLA;  
 RX MEDLINE=94105324; PubMed=8278528;  
 RA Poulson P., Kreiberg J.D.;  
 RA "Starch branching enzyme cDNA from Solanum tuberosum.";  
 RL Plant Physiol. 102:1053-1054(1993).  
 RN [2]  
 RP SEQUENCE OF 279-527 FROM N.A.  
 RC STRAIN=CV. DESIREE; Tissue=Tuber;  
 RX MEDLINE=92079917; PubMed=1745241;  
 RA Kosmann J., Visser R.G.F., Mueller-Roeber B., Willmitzer L.,  
 RA Sonnwald U.;  
 RT "Cloning and expression analysis of a potato cDNA that encodes  
 RT branching enzyme: evidence for co-expression of starch biosynthetic  
 RT genes.";  
 RL Mol. Gen. Genet. 230:39-44(1991).  
 CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF  
 CC STARCH.  
 CC -1- PATHWAY: THIRD STEP IN STARCH BIOSYNTHESIS.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SURCELLULAR LOCATION: AMYLOPLAST.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO  
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.  
 CC  
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 CC  
 CC DR EMBL; X69805; CAA49463.1; -  
 CC DR PIR; S18594; S18594.  
 CC DR Mendel; 13376; Soltu; Sbel.1.  
 CC DR InterPro: IPR000461; -  
 CC DR Pfam: PF00128; alpha-amylase; 1.  
 CC Starch biosynthesis; transferase; glycosyltransferase; Amyloplast.  
 CC ACT\_SITE 424 424 BY SIMILARITY.  
 CC ACT\_SITE 484 484 BY SIMILARITY.  
 CC ACT\_SITE 553 553 BY SIMILARITY.  
 CC FT SEQUENCE 861 AA; 99083 MW; F3D519AC7CF1BEF2 CRC64;

Query Match 47.2%: Score 2145; DB 1; Length 61;  
 Best Local Similarity 51.6%; Pred. No. 3.8e-148;  
 Matches 411; Conservative 116; Mismatches 183; Indels 86; Gaps 12;

34 LSFNR-----EAFSRVFGSKSSH-----ESDSSTVAVYTSKR 67  
 1 MEINRVLVSLKPIRGSPFSPKVSASGRNKICFSGHSTGLKSGQSRSMWISTPKSR 60  
 68 VLDPGRICEYSSSTQLEAPGVSESOYLDVDELIMDKIVEDEVKESVPHREYSI 127  
 61 VRKDERMK-HSSAI-----SAVLID-----DSTYMAPLEEDYKT 93  
 128 RKIGSKRSPISPPGRCQRIYDIPSTFGRHLDYRYSQYKRLREIDKYEISIDAFSRG 187  
 94 ENIG-----LNLDPLEPLIDFHRHMRKRYDOKMLKLEIYELPLEEFAOG 139  
 188 YEKFGSRSETGITYREMAPGATWALLIGDENMNPADVMTONEGCVWEIYLPNNDGS 247  
 140 YLKFGNREDGCIYREMAPGAEDEVIGDFGNWNGSNHMEKIDFGWISIVIP-DVSK 198

OY	248	PIIPGSGKIMLMDPSSGN-KDSIPAMKFEVQAAGEL--PYNLIYYDDPEEKEYYVKNP	304
Db	199	PVPIPNSSKVKRFRKKGNSGWMDRIPAMIKYATATATATFAPADGVYWDPPSESEYHKKYP	258
OY	305	QPKRKRSLRIEESHGMSSTEPVINTYANFPDVLPRIKLGVNAVOLAIOEHSYASF	364
Db	259	RPKPRADRIAYEAHGMSSSPREVNSYREFADVLPRIKANNNTYVGLAIMEHSYGSF	318
OY	365	GYYHTNFEFAVSSRGCTPDDKLSLIDKAHELGLVLMDIVSHSHASTNGLDGLNFD--GT	421
Db	319	GYYHTNFEFAVSSRGPNPDLKYLIDKASHSLGLVAVLVVSHSHANNYDGLNGFDIGQGS	378
OY	422	DGHYHSPRGCHMMHMDSLRFLFNYSWEVLRLFLSNARWMLDEYKFDGCFRFDGYTSMAYTH	481
Db	379	QESIFHAEGRGHKLMDSLRLFTYANWEVLRLFLSLNLRWMLDEYKFDGFRDGYTSLMYH	438
OY	482	HGLQVDFGNTNNEYGYATPDVAVVYLMLLNDMLHGLFEPAVTIGCEVSGMPVTCIPVED	541
Db	439	HOINNGFIGNTNEYSEATDVAVYLLMLANLLHKKIFPDATVYIAEDVSGMPGLGRVSE	498
OY	542	GGVGFDFRLHMAVADKVEIIO-KREDEMKGDIVHMLTNRMLKEKCVSYAESHDAQLVG	600
Db	499	GGIGFDYRLAIPDKWIDYLLKNKDEWDSMKEVTSITNRRYREKCIAYAESHDQITVG	558
OY	601	DKTIAFWLMDMDYDFMALDPRSPFLDLRGALHKKMIRLITMGIGGGGYLNFPGNENGHP	660
Db	559	DKTIAFLFLMDKEMYSGMSCLDASPDVYDRJALHKKMHFFLMALGGGGYLNFMKNEGHPR	618
OY	661	EWIDEPBGDLHLPQKGFVPGNNYSYDKCRRPFDGNSKHLRYHGMQEPDAIOHLEBAYG	720
Db	619	EWIDEPB-----EGNMSTYDKCRKRWMLADSEHLRYKRMANFDRAMNSLDKFS	667
OY	721	FMTSEHOYISKDERDRIIVEERGNLVFVFNFWHTSSYSDYRVGCLKPGYKKTIVLSDDP	780
Db	668	FLASGKQIVSSMDMDKNKVVYEREDLVFVFNFWHTKNTYEGYKVCGLDPRKYVALDSDAW	727
OY	781	LEGGGRSLSHDAEHS 796	
Db	728	EFGGGRGTGHVDHPT 743	
RESULT 3			
GLGB_ORYSA	STANDARD:	PRT:	820 AA.
AC	001401;		
DT	01-JUL-1993 (Rel. 26, Created)		
DT	01-JUL-1993 (Rel. 26, last sequence update)		
DT	01-NOV-1997 (Rel. 35, last annotation update)		
DE	1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (STARCH BRANCHING		
DE	ENZYME) (Q-ENZYME).		
GN	SBE1.		
OC	Oryza sativa (Rice).		
OC	Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta;		
OC	Magnoliophyta: Liliopsida, Poales; Poaceae; Ehrhartoideae; Oryzae;		
OC	Oryza.		
OX	NCBI_TaxID=4530;		
RN	SEQUENCE FROM N.A.		
RP	STRAIN=CV_JAPONICA; TISSUE=Endosperm;		
RA	Nakamura Y., Yamanouchi H.;		
RT	"Nucleotide sequence of a cDNA encoding starch-branching enzyme, or		
RT	Q-enzyme I, from rice endosperm.";		
RL	Plant Physiol. 99:1265-1266(1992).		
RN	SEQUENCE FROM N.A.		
RX	MEDLINE=93204882; PubMed=8455548;		
RA	Kawasaki T., Mizuno K., Baba T., Shimada H.;		
RT	"Molecular analysis of the gene encoding a rice starch branching		
RT	enzyme.";		
CC	Mol. Gen. Genet. 237:10-16(1993).		
CC	-1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF		
CC	GLYCOGEN.		
CC	-1- PATHWAY: THIRD STEP IN STARCH BIOSYNTHESIS.		

CC	-1	SUBUNIT: MONOMER.	
CC	-1	SUBCELLULAR LOCATION: AMYLOPLAST	
CC	-1	SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.	
CC		-----	
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation - the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/notice/ib-sib.ch/">http://www.isb-sib.ch/notice/ib-sib.ch/</a> ).	
CC		or send an email to <a href="mailto:license@ib-sib.ch">license@ib-sib.ch</a> ).	
CC		-----	
DR	EMBL; D10752; BAA01584.1; -.		
DR	EMBL; D10838; BAA01616.1; -.		
DR	InterPro; IPR000461; -.		
DR	Pfam; PF00128; alpha-amylase; 1.		
KW	Starch biosynthesis; Transferase; Glycosyltransferase; Amyloplast.		
FT	MOD_RES	1	BLOCKED.
FT	ACT_SITE	409	BY SIMILARITY.
FT	ACT_SITE	464	BY SIMILARITY.
FT	ACT_SITE	533	BY SIMILARITY.
FT	CONFLICT	13	P -> A (IN REF. 2).
FT	CONFLICT	715	VGHVDHPTSEGGNGVETENFNRRNSFKVLSPPRCV -> LAMWITSRIRPREGCEYQKQISTALATHSKSPRRV
FT			PVM (IN REF. 2)
SEQUENCE	820 AA; 93262 MW; A687CF936F359DF CMC64;		

Query Match	46.9%	Score 2130.5	DB 1	Length 820
Best Local Similarity	54.5%	Pred. No. 4e-147		
Matches	401	Conservative 113	Mismatches 171	Indels 51
			Gaps	11
QY	132	SKPR-----SIPPGRGQR-----	TYDPSLTGFRQHDLYRSGY	167
Db	40	SSPRSMGPKVYKTNPSVATARKNKTMTVVEVDHLIYDLPDLKEFKHFNRIKRY		99
QY	168	KRLREIDIKYESLDAFGRGYEKEPFSSENGITRYREMAPGTMYALLGDFPNMNPMDV		227
Db	100	LDQCLIRKHHSGLEEFSESGYLKFGSINTVVGATTYIREMAPAOEQALLGEEFPNNMGAKHK		159
QY	228	MTQNGCEWAEIFLPNNADSGPRIPGSHVKYIKMDPDSGN-KDPSIAWTKFSVOAREGL--		284
Db	160	MEKDKFGIMSTKI-SHVNGKRALPNSKVYKFRFRGGGAWMDRIAPAWIRYATFPAKSKGA		218
QY	285	PLNGIITYRPREPEEKVYFKNPQPRKRSIRIYESHVGMSSTEVINTYANFRDQVLPRIKK		344
Db	219	PYDGHMPPACERFYVFNHPRPKEDARIRYEAHVGMSGESEVSTYREFADNVLPRIIRA		278
QY	345	LGYNVQVLMALIOEHSYKASFGYHVNFFPAASSRGETPDLKSLDKARELIGLYLMDIVH		404
Db	279	NNYNTVQVLMALIEHSYKASFGYHVNFFPAASSRGETPDLKSLDKARELIGLYLMDIVH		338
QY	405	SHASTNTLDGIMLP-GADNH--YHSGSPRGHHMMWMDRLFNYSGEWLYRFLLSNARWL		461
Db	339	SHASNNTVDGLNGVGVGQNTHESYHNTDRCYHKLMDSRLFNYSANWEVLYRFLLSNLRYYM		398
QY	462	DEYKDKGRFRDQVYTSMMATTHHSGLOYDFGNGTNEYRGYATIDVDVAVYLMALMDIHGLEPPE		521
Db	399	DEFMDDGRFRDQVTSMLNHHHNGKNGKKEYPSLTDVDAIYYKMLAHNLHMKLPE		458
QY	522	AVTIGEDVSGMPTVCIPEDGCGVGFYRLHMAVAARKVEIIO-KRDEPMKGGDIYHMLTJN		580
Db	459	ATIVAEVDGSGMPTVLCRPDDEGCGVGFDFLMAAIPRWMLIDLYLNKKDKRMSHSEIYQITLTN		518
QY	561	RRWLECVSYAESHDOALVGDKTIAFWMLDKDMYDEMALDRSTPLIDRGVALHKKMPLI		640
Db	519	RRYTEKCAIYAESHSQSIYVGDKTIFALLMDKEMYTGMGSDLOPASPITNKGTAOLKIMIFI		578
QY	641	TMGGGEGEYLNDPMGNEPFRPMIDPRDDIHLPSKFTVPGNNYSYDCKRRRFPDLSGNSHT		700
Db	579	TMAJGGDITLNDPMGNEPFRPMIDPR-----EGNNWSTDKCKRQWSTLVDDIHL		627



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OY 701 RYHMOEFDALIOHLEAYGFMTESEHOYISRKDERBRIYERNGNLVFNFMHTSYSD 760
DB 628 RYKMNAPDQMMNLEEFSSKQIVSDMKNKVIYFERQDLVFNFMHTSYSD 687
OY 761 YRVCGLKPKKRYIVDDPFGFGRSLSDAENF-SPEGM-----YNNRPSFVYIT 812
DB 688 YKVCDDLEKRYVALDSDALVGGHGVHDVHTFSPGKPVETNNRPSFVYIT 747
OY 813 PCRTAVYALVEDEVE 828
DB 748 PPRTCVAYRVEDRE 763

RESULT 4
GLGB_HUMAN STANDARD; PRT; 702 AA.
ID GLGB_HUMAN
AC 004446;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE 1.4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOGEN BRANCHING
ENZYME) (BRANCHER ENZYME).
GN GBEL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Thon V.J., Khaili M., Cannon J.F.;
RT Isolation of human glycogen branching enzyme cDNAs by screening
RT complementation in yeast.
RL J. Biol. Chem. 268:7509-7513(1993).
CC -1- FUNCTION: REQUIRED FOR SUFFICIENT GLYCOGEN ACCUMULATION. THE
CC ALPHA 1-6 BRANCHES OF GLYCOGEN PLAY AN IMPORTANT ROLE IN
CC INCREASING THE SOLUBILITY OF THE MOLECULE AND, CONSEQUENTLY, IN
CC REDUCING THE OSMOTIC PRESSURE WITHIN CELLS.
CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF
CC GLYCOGEN.
CC -1- PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.
CC -1- SUBUNIT: MONOMER.
CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN LIVER AND MUSCLE.
CC -1- DISEASE DEFECTS IN GBEL ARE THE CAUSE OF GLYCOGEN STORAGE DISEASE
CC IV (GSD-IV) (ALSO KNOWN AS ANDERSEN'S DISEASE): A RARE FORM OF
CC GLYCOGENOSIS CHARACTERIZED BY THE ACCUMULATION OF ABNORMALLY
CC STRUCTURED GLYCOGEN THAT RESULTS IN EARLY ONSET HEPATIC CIRRHOSIS,
CC CARDIAC ARREST AND NEUROMUSCULAR DISEASES. MOST CHILDREN WITH THIS
CC CONDITION DIE BEFORE TWO YEARS OF AGE. NO TREATMENT APART FROM
CC LIVER TRANSPLANTATION HAS BEEN FOUND TO PREVENT PROGRESSION OF THE
CC DISEASE.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL: L07956; AAA58642.1; -
DB MIM: 232500; -
DB InterPro: IPR000461; -
DB Pfam: PF000128; alpha-amylase; 1.
DB Glycogen biosynthesis; Transferase; Glycosyltransferase;
DB Glycogen storage disease.
DB ACT_SITE 357 357 BY SIMILARITY.
DB ACT_SITE 412 412 BY SIMILARITY.
DB ACT_SITE 481 481 BY SIMILARITY.
DB SEQUENCE 702 AA; 80443 MW; 4DF3AABD363A8FE3 CRC64;

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Query Match 45.1%; Score 2049; DB 1; Length 702;
Best Local Similarity 55.1%; Pred. No. 2,76-141;
Matches 376; Conservative 117; Mismatches 174; Indels 16; Gaps 5;

OY 145 RIYIDPSTLGRQHLIDYISQYKRLREIDIXYBESLAFSGYKRGQFSR-SEGIYTR 203
DB 30 RLEIDPVLKPAVDFOFYRKQPSQLTKWIGNEBGIDFSGYKRGQFSR-ADGGLYSK 89
OY 204 EWAPGATMAALIGDENNNPNADVMTQNECGWEIIFLEPNADGSPPIPHGSHVTRMDTP 263
DB 90 EWAPGEGVELTDFGNGMPSFYRKLDYQWELTYIPKOKRSVLPVPHSGSLKLYITSK 149
OY 264 SGN-KDSIPAWIKFSVOAGELPYNQIYDDPREBEERYKFNQPRKPSLRJYESHWMS 322
DB 150 SEGLTYRISPMKAYVYREGDNVNYDMIMWD--EHSYEFKHSRPRKPSLRJYESHWIS 207
OY 323 STEPVNTYANFRDVLPRIRKILGYNAVQVMAIOHSHYASRGYVHTFYAASSHFGTDP 382
DB 208 SHRGKVASYKHFQCNVLPRIKIGYNCIQVMAIMHAYASRGYQITSFPAISRYGTPE 267
OY 383 DLKSLDKAHEILGYLVMDIVHSHASTNTLDGLNPDGDDGYFSPGRGHMMDSRLF 442
DB 268 ELQELVDTHSMGIYLLDVVSHASKNSADGLNPFDDGSCYFHSRGTDLMDSDRLF 327
OY 443 NGCSWEVLFLLSNARWVDEKFGFGRDGYTSMKTYHHGLQVDFGNYNFEGYATDV 502
DB 328 AYSSWEVLFLLSNARWVDEKFGFGRDGYTSMKTYHHGLQVDFGNYNFEGYATDV 387
OY 503 DAVVYLMINDMIGLEPRAVTIGEDVSGMPVCIPEVDGCVGDFYRLMAVADKWEIT 562
DB 388 DALTYTLMANHHVHTLCPSITIAEDVSGMPALCSIGSGGGEFYRLAMAPDWIDL 447
OY 563 OK-RDEDMKMGDIVHMLTTRRMLEKCVSAESHDAOLVGDKTIAFWLMDKDYDFMALDR 621
DB 448 KERKDDMMNGDIVYLLTTRRMLEKCVSAESHDAOLVGDKTIAFWLMDKDYDFMALDR 507
OY 622 PEPPLDRCVALHKKMRLITLTMGLGEGYLNFGNFGHPEWIDFPRGDLHL-SGKFGVN 681
DB 508 PEPVYIDRIGLQKMKRILTLTHGLGEGYLNFGNFGHPEWIDFPR-----SGN 556
OY 682 NYSYDCRRRFDGNSKHLRYHGMQFDOALIOHLEAYGFMTESEHOYISRKDERIYFV 741
DB 557 NESYHARRQFHLTDODLLRYKFLNPFCDMNRLEBERGVMLAAPAVYSEKHEGKIIAF 616
OY 742 ERENLYFVFNFMHTSYSDRYGCLKPGKRYKTVLSDPDLFGFGRSLSDAIFHSEFGNY 801
DB 617 ERKGLFIFNFMHTSYSDRYGCLKPGKRYKTVLSDPDLFGFGRSLSDAIFHSEFGNY 676
OY 802 DNPRPSFVYITCKRTAVYALVE 824
DB 677 NGRPYSILVYITPSRYVALIQLNVD 699

RESULT 5
GLGB_YEAST STANDARD; PRT; 704 AA.
ID GLGB_YEAST
AC P32775;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE 1.4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOGEN BRANCHING
ENZYME).
GN GIC3 OR YEL011W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92340578; PubMed=1634552;
Thon V.J., Vigneron-Lesens C., Marianne-Pepin T., Montreuil J.,

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RA Deog A., Rachez C., Ball S.G., Cannon J.F.:  
 RT "Coordinate regulation of glycogen metabolism in the yeast  
 RT *Saccharomyces cerevisiae*. Induction of glycogen branching enzyme.";  
 RL J. Biol. Chem. 267:15224-15228(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN: S288C / AB972;  
 RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,  
 RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,  
 RA Chung E., Duncan M., Guzman E., Hartzell G., Hunkle-Smith S.,  
 RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,  
 RA Meschede D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,  
 RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,  
 RA Taylor P., Wei Y., Yellon M., Botstein D., Davis R.W.:  
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF  
 CC GLYCOGEN.  
 CC -1- PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING THE TRANSITION BETWEEN THE  
 CC LATE EXPONENTIAL AND STATIONARY GROWTH PHASES, COINCIDENT WITH  
 CC MAXIMAL GLYCOGEN ACCUMULATION.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO  
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: M76739; AAA34632.1; -  
 DR EMBL: U18530; AAB64488.1; -  
 DR PIR: A42752; A42752.  
 DR SGD: S0000737; GLC3.  
 DR InterPro: IPR000461; -  
 DR Pfam: PF00128; alpha-amylase; 1.  
 DR GlycoGen biosynthesis; Transferrase; glycosyltransferase.  
 FT ACT\_SITE 356 356 BY SIMILARITY.  
 FT ACT\_SITE 417 417 BY SIMILARITY.  
 FT ACT\_SITE 486 486 BY SIMILARITY.  
 FT CONFLICT 564 564 S -> T (IN REF. 1).  
 SQ SOURCE 704 AA; 8115 MW; 9C2227E107B825F27 CRC64;

Query Match 38.8%; Score 1765.5; DB 1; Length 704;  
 Best Local Similarity 50.6%; Pred. No. 1,1e-120;  
 Matches 367; Conservative 109; Mismatches 190; Indels 59; Gaps 19;

QY 136 SIPPGRGQRIYDIDSLGFRQHLDRYSQKRLREIDKY-----EGSIDAFSR 186  
 DB 3 NIDDNKKG-AVEFDPLWLPFADYLSER-----RYLADKLYDTHTATPGSQSLSK 53  
 QY 187 -----GYEKGF-SRSEPT-GITTYREMAPGATMAALIGDFNNMNPNA-DVATONCEGCVET 239  
 DB 54 FARDSKYSGLAHNPETKEITKYEMAPNAREFIVGDFNMOTTHHELNKDNDEGNFTIT 113  
 QY 240 LPPNAGSGPPIPHGSRVYKTRMOTPSGNK-DSIPAMIKFSVQAPGEL-----PYNGIYD 292  
 DB 114 LHPDLPNGDPAIPDPSKIKWFIPLPGSKIFRLPAMITRATOPSKETSKOGFAVEGRWN 173  
 QY 293 PPEEEKYFKNPQPRPK---SLRIYESHVGVSSPEPIYNTYANRDYVLRIRKLGNA 349  
 DB 174 P--ENYKYVHPKPKSEVSDSLRIYEAHVIGSSPEKITTYKTEKTEVLPRIKYLGA 231  
 QY 350 VOLMAIQEHSYASFGYHTNFYFASRRGTGPDLSKLIDRAHEGLGLVLDIYHSHAST 409  
 DB 232 IQMAIMEAHAYVASRGYQTNFFAASSRGCEELKEKELIDRAHSGILVLDVYHSHASK 291  
 QY 410 NPLDGLNMFDDGDTGATFH--SGPRGHMMWDSRLFNYSWEVLRLSLNARWMLDEKFD 467  
 DB 292 NVEDGLNMFDDGDTGATFH--SGPRGHMMWDSRLFNYSWEVLRLSLNARWMLDEKFD 351

QY 468 GRPDGVTSMATYTHHGLGV--DEFGNNEYFG---YATDVAVVYIMLNDMTHGLPPE- 521  
 DB 352 GRPDGVTSMYVHGVGAGGSGFSGDYNEYLSDRSRSPVDEHALAYIMLNDLVHEMLPVL 411  
 QY 522 AVTIGEDVSGMPYCIPIPDGSGVGFDRILMAVADKVEII-QKREDBKMGDIYMLTN 580  
 DB 412 AVTAEDVSGPPTLCPLPSIGTGFDYRLMALPDMWIKIKLKKEKDEDEMSIYVTLTN 471  
 QY 581 RRMLEKVSVAESHDQALVGDPTAFWIMDKMY-DEMALDRSEPTDILRGVALHMKRL 639  
 DB 472 RRYGKVAVACESHDQALVGDPTAFWIMDKMY-DEMALDRSEPTDILRGVALHMKRL 530  
 QY 640 ITMGLGEGYITNFGNNEGHPEWIDPRGLHLPSEKVEYGNYSYDKORRRDLGNSKH 699  
 DB 531 ITHSLGGEAYINFGNNEGHPEWIDPRGLHLPSEKVEYGNYSYDKORRRDLGNSKH 579  
 QY 700 LRYHGMQEPDQALHLEAVGFMTESEHQYISKRDERDRIYFERGLVYVFNHMTSSS 759  
 DB 580 LRYONLEFDSKQWCKRHRKWLTKQAYVSLKHEDDKMIVFERNNLFIYFNHMTSSS 639  
 QY 760 DYRGCLPKPKYKIVLDSDDLFGFGFRLSHDAEHSFEGWYDNRPSMVTTPCPTAVY 819  
 DB 640 DYRGVAKAGHYHIVLNSDRAEFGGHNRIKINSESEFTTDLKNNKNEFLQVYIPSRVALY 699  
 QY 820 YALVE 824  
 DB 700 LALKE 704

RESULT 5  
 ID GLGB\_SYNP7 STANDARD; PRT; 773 AA.  
 AC P16954;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE 1.4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOGEN BRANCHING  
 ENZYME).  
 GN GLGB.  
 OS *Synechococcus* sp. (strain PCC 7942) (*Anacystis nidulans* R2).  
 OC Bacteria; Cyanobacteria; Chroococcales; *Synechococcus*.  
 OX NCBI\_TaxID=1140;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90323609; PubMed=2142668;  
 RA Kiel J.A.K.W., Boels J.M., Belman G., Venema G.:  
 RT "Nucleotide sequence of the *Synechococcus* sp. PCC7942 branching  
 RT enzyme gene (glgB): expression in *Bacillus subtilis*.";  
 RL Gene 89:77-84(1990).  
 CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF  
 CC GLYCOGEN.  
 CC -1- PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- MISCELLANEOUS: THE TEMPERATURE FOR OPTIMAL ACTIVITY IS  
 CC APPROXIMATELY 35 DEGREES CELSIUS.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO  
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: M31544; AAB39038.1; -  
 DR PIR: J00550; J00550.  
 DR InterPro: IPR000461; -  
 DR Pfam: PF00128; alpha-amylase; 1.  
 KW GlycoGen biosynthesis; Transferrase; glycosyltransferase.  
 FT INIT\_MET 0 0



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 7, 2001, 11:17:58 ; Search time 31.12 Seconds

(without alignments)  
3554.210 Million cell updates/sec

Title: US-09-297-703A-29

Sequence: 1 MGRHTTSGIRPPCAPLCKSQ.....AVYALVEDEVNLEPFAV 836

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 425026 seqs, 133305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP-archaea:.\*  
2: SP-bacteria:.\*  
3: SP-fungi:.\*  
4: SP-human:.\*  
5: SP-invertebrate:.\*  
6: SP-mammal:.\*  
7: SP-mhc:.\*  
8: SP-organelle:.\*  
9: SP-phage:.\*  
10: SP-plant:.\*  
11: SP-rodent:.\*  
12: SP-unclassified:.\*  
13: SP-vertebrate:.\*  
14: SP-virus:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3482.5	76.6	870	10 Q9XIS5	Q9XIS5 phaseolus v
2	3467	76.3	922	10 Q41058	Q41058 pisum sativ
3	3384.5	74.5	800	10 Q42531	Q42531 arabidopsis
4	3384.5	74.5	805	10 Q9LZS3	Q9LZS3 arabidopsis
5	3381.5	74.4	878	10 Q9XGA6	Q9XGA6 solanum tub
6	3373	74.2	858	10 Q23647	Q23647 arabidopsis
7	3360	73.9	871	10 Q9XGA5	Q9XGA5 solanum tub
8	3356	73.8	882	10 Q9XGA8	Q9XGA8 solanum tub
9	3343	73.5	830	10 Q49953	Q49953 solanum tub
10	3340	73.2	854	10 Q9XGA7	Q9XGA7 solanum tub
11	3327	72.2	854	10 Q42526	Q42526 arabidopsis
12	3315	71.8	814	10 Q9XGA9	Q9XGA9 oryza sativ
13	3261.5	71.7	823	10 Q24421	Q24421 zea mays (m
14	3260.5	71.6	823	10 Q9F007	Q9F007 triticum ae
15	3254.5	71.0	734	10 P93691	P93691 triticum ae
16	3225	70.6	729	10 Q9ZPB7	Q9ZPB7 hordeum vul
17	3209	70.0	825	10 Q24397	Q24397 triticum ae
18	3180	69.7	799	10 Q40663	Q40663 oryza sativ
19	3169	69.7	799	10 Q81387	Q81387 zea mays (m

20	3152.5	69.4	829	10 Q9ZTB6	Q9ZTB6 hordeum vul
21	2180	48.0	830	10 Q04864	Q04864 solanum tub
22	2165	47.6	810	10 Q9XGB3	Q9XGB3 triticum ae
23	2163	47.6	830	10 Q04074	Q04074 triticum ae
24	2163	47.6	833	10 Q9XGB1	Q9XGB1 triticum ae
25	2163	47.6	833	10 Q9F008	Q9F008 triticum ae
26	2163	47.6	865	10 Q9XGB2	Q9XGB2 triticum ae
27	2159	47.5	852	10 Q08131	Q08131 manihot esc
28	2143	47.2	832	10 Q9M6P8	Q9M6P8 sorghum bic
29	2134.5	47.0	847	10 Q9XIS4	Q9XIS4 phaseolus v
30	2130.5	46.9	820	10 Q40664	Q40664 oryza sativ
31	2124	46.7	823	10 Q41740	Q41740 zea mays (m
32	2107	46.4	807	10 Q9XED2	Q9XED2 triticum ae
33	2091.5	46.0	829	10 Q9XED3	Q9XED3 aegilops sat
34	2072.5	45.6	826	10 Q41059	Q41059 pisum sativ
35	1999	44.0	686	3 Q9Y8H3	Q9Y8H3 emeritella
36	1987	43.7	766	10 Q49185	Q49185 gracilaria
37	1976.5	43.5	733	3 Q9P5P3	Q9P5P3 neurospora
38	1897.5	41.7	865	5 Q9V6K7	Q9V6K7 drosophila
39	1885	41.5	681	5 Q22137	Q22137 caenorhabdi
40	1487	32.7	686	10 Q24393	Q24393 triticum ae
41	1351.5	29.7	433	10 Q9XGA9	Q9XGA9 solanum tub
42	1298	28.6	903	10 Q9LTP8	Q9LTP8 arabidopsis
43	778	17.1	190	10 Q9T0N3	Q9T0N3 solanum tub
44	769	16.9	189	10 Q9T0N2	Q9T0N2 solanum tub
45	669.5	14.7	187	10 Q9SSX6	Q9SSX6 nicotiana t

## ALIGNMENTS

RESULT	1	ALIGNMENTS
Q9XIS5	PRELIMINARY;	PRT; 870 AA.
ID Q9XIS5	Q9XIS5	
AC Q9XIS5	Q9XIS5	
DT 01-NOV-1999 (TRENBLER, 12, Created)		
DT 01-NOV-1999 (TRENBLER, 12, Last sequence update)		
DT 01-MAR-2001 (TRENBLER, 16, Last annotation update)		
DE BRANCHING ENZYME 1 PRECURSOR (EC 2.4.1.18).		
GN KBE1.		
OS Phaseolus vulgaris (Kidney bean) (French bean).		
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;		
OC Fabales; Fabaceae; Papilionoideae; Phaseolus.		
OX NCBI_TaxID=3885;		
RN [1]		
RP SEQUENCE FROM N.A.		
RA Nozaki K., Ito H., Matsui H., Honma M.;		
RT "Phaseolus vulgaris L. mRNA for starch branching enzyme 1.";		
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.		
DR EMBL: AB029548; BAA82348.1; -		
DR InterPro: IPR000461; -		
DR Pfam: PF00128; alpha-amylase; 1.		
KW Transl. peptide; Transferase; Glycosyltransferase.		
KW TRANSIT 1		
FT POTENTIAL.		
SQ SEQUENCE 870 AA; 98890 MW; BDB5C0289B6694EC CRC64;		

Query Match	76.6%	Score 3482.5;	DB 10;	Length 870;
Best Local Similarity	73.9%	Pred. No. 1.2e-251;		
Matches 645; Conservative 79; Mismatches 96; Indels 53; Gaps 6;				
QY 4 YTGIRPPCAPLCKSQSTGFHGRVTSCTSEFNKFAFRVSKSGSHSSSNVMT 63				
DB 3 YTGIRPPCAPLCKSQSTGFHGRVTSCTSEFNKFAFRVSKSGSHSSSNVMT 60				
QY 64 ASKRVLPDGRICYSSTQLEAPGVSESYVLTVESLIMDKIYEDS----- 113				
DB 61 ESDRVLPDGRICYSSTQLEAPGVSESYVLTVESLIMDKIYEDS----- 112				
QY 114 -----VKSESVPAREYSIKTSKRSRSTPPRGRIYDIP 151				
DB 113 SYRIEDGLGSSVSPVDVDPAPKRTSVGKVKIPISVPAKRTIPRPGAGKIYEDIP 172				

QY	152	SLIGRCHLDYRQYKRLREIDIKYEGSLDASRKYETKGFSGSSEGTITYYREMAPATM	211
Db	173	SLAYRDLDRDQYKRLHDEIKKHREGLDASRSGDEQEFLLSAGITGIRREMAPAKS	233
QY	212	ALLIGDENNNPNADVMTQNECGWEIETLPNNADGSEPPIPHGSRVKITRMOTPSGNKDISP	271
Db	233	ALLIGDENNNPNADVMTRNEFGWEIETLPNNADGSPPIPGSVKIRIMOTPSGKDISP	292
QY	272	AMIFRSVOAPELDELYNGIYDPRPEEKYVFNKPDQPKRKSRLRIESHVGMSSTEPVINTY	331
Db	293	AMIFRSVOAPELDELYSGIYDPRPEEKYVFNKPDQPKRKSRLRIESHVGMSSPEPKINTY	352
QY	332	ANFRDDVLPRIKKTGYNAVQMLALQIESHSYVSFCGYHTNFPAASSRGTGTDLKSILDKA	391
Db	353	ANFRDDVLPRIKKTGYNAVQMLALQIESHSYVSFCGYHTNFPAASSRGTGTDLKSILDKA	412
QY	392	HELGLIYVIMODIVHSHASNTLIDGLNMPDGTGCHYFHSRPGRHMMMDSRLEFNGSMWYLR	451
Db	413	HELGLIYVIMODIVHSHASNTLIDGLNMPDGTGCHYFHSRPGRHMMMDSRLEFNGSMWYLR	472
QY	452	FLLSNARWMLDEYKFDGFRPGVATSNMATHHGLQVDPFGNNEFYGATVDVAVYVLM	511
Db	473	YLLSNARWMLDEYKFDGFRPGVATSNMATHHGLQVDPFGNNEFYGATVDVAVYVLM	532
QY	512	NDMIHGLFPEAVTIGEDVSGMPYVCIPVEDGGVGVDYRLHMAVADKWEYITIQKDEDMKM	571
Db	533	NDLIHGLFPEAVTIGEDVSGMPYVCLPQDDGVGVDYRLQMALADKWEITELIKODEDMKM	592
QY	572	GDIYHMLTNRRMLEKCVSAYASHDQALVGDKTIAFWMLDKDMYDFMALDRSTPLIDRGV	631
Db	593	GDIYVTLTNRRMLEKCVAYASHDQALVGDKTIAFWMLDKDMYDFMALDRPATRIDRGI	652
QY	632	ALHKMIRLITLIGLGGEGYLNMGNEFGHPENKIDPRGDLHLSRKFYVGNVSYDKCRR	691
Db	653	ALHKMIRLITLIGLGGEGYLNMGNEFGHPENKIDPRGDLHLSRKFYVGNVSYDKCRR	712
QY	692	FDLGSKTLRKHGMQEFQOALQHLHEAAGFMTSEHOYSRSRDESDRLITVEFGMLVJVFN	751
Db	713	FDLGSKTLRKHGMQEFQOALQHLHEAAGFMTSEHOYSRSRDESDRLITVEFGMLVJVFN	772
QY	752	FHMNYSYSDYVGGCCKPKKYKIVLSDDDPLRGGGGRGSHDHEFSPGQYNNRPSRFVY	811
Db	773	FHMNYSYSDYVGGCCKPKKYKIVLSDDDPLRGGGGRGSHDHEFSPGQYNNRPSRFVY	832
QY	812	TPCRATVYVALE-----DEVE---NELEP	833
Db	833	APSRATVYVALEDDLEPAFDEVEPALADEVBP	865
RESULT	2		
Q41058			
Q41058	PRELIMINARY:	PRT:	922 AA.
NC	Q41058:		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)		
DE	STARCH BRANCHING ENZYME I PRECURSOR.		
GN	SBEI OR SBEI.		
OS	Plum sativum (Garden pea).		
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;		
OC	Fabales; Fabaceae; Papilionoideae; Plsum.		
OC	NCBI_TaxID=3888;		
RM	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=95201826; PubMed=7894509;		
RA	Burton R.A., Bewley J.D., Smith A.M., Bhattacharyya M.K., Tatge H.,		
RA	Ring S., Bull V., Hamilton W.D.O., Martin C.;		
RT	"Starch branching enzymes belonging to distinct enzyme families are		
RT	differentially expressed during pea embryo development."		
RL	Plant J. 7:3-15(1995).		
DR	EMBL; X80009; CAA56319.1; -		

DR	Mendel, 16398; Piasa; Sbel, 16398.
DR	InterPro, IPR000461; -, -
DR	Flam; PF00128; alpha-amy, 1.
KW	transit peptide.
TRANSIT	1
FT	48
CHAIN	922
SEQUENCE	922 AA: 105227 MW: 4EDBF9374C6385C8 CRC64:
	POTENTIAL.

Query Match	76.38%	Score 3467	DB 10	Length 922
Best Local Similarity	75.68%	Pred. No. 2e-250		
Matches 647	Conservative 76	Mismatches 97	Indels 36	Gaps 9

QY	4	YTGSGIRPPQAP-LJCKGOSJTGFBHRTSSQJLS- -NFKFEJSPRRVSGKSSHIESOSJNV	60
Db	3	YTISSIRPPVLPJSLHKST- --LRODRASSHSIFPLKNNSSSFWSJLXAFNSHSEFKSS	59
QY	61	MYTASRKVLPGRJECJSSSSJTDQLEAPGYSEBQOJLVTPESLIMD- - - - -	107
Db	60	TIASBCKVLIPEDODNSVSLDQJLENPEDITSBQO- --NLEDLTKRGKNTN'DESRST	116
QY	108	KRIVEDE- - - - -VNKESVPMRETV- SIKRIG- SKRPSIDPPREGORTY'DIDBSLT	154
Db	117	REYGEKGSVTSSSLVJNDVTQJAKKTSVSHDKKVVKKDKRPIITPPEGTGKI'ETIDPLIO	176
QY	155	GFRQHLDRYQOYKRLREJIDKYGSLDAESRGEKTFGSKSETGTIYREMAVQATWAL	214
Db	177	AHROHLDRYQOYKRIREJIDKYGEGJDAFSRGEKTFGFSRAGIYREMAVQASAL	236
QY	215	IGDFNNMPPNADVMTQNCGQWAEJFLPNMADGSPRIPHGSKVKITMDTPSGMNDSDIPAWI	274
Db	237	VGDFNNMPPNADVMTKDAFGWAEJFLPNMADGSPRIPHGSKVYKIHMDTPSGIIDSIPAWI	296
QY	275	KFSVQAPGELPRNGIYUYPPEEEKYVFENPDQPKPKSLRIYIESHVGSSTEPJYINTYANF	334
Db	297	KFSVQAPGEIIFYNGIYUYPPEEEKYVFENHPQPKRQOSIRIYIESHIGSSDEPIKINTYANF	356
QY	335	RDDVPLR'IKKIGYANVQOMAJOEHSYASFGYHTNTNYAASSRPGTDDKLSJLDRKHNL	394
Db	357	RDDVPLR'IKKIGYANVQ'IMAJOEHSYASFGYHTNTNFAPSSRPGTDEDKLSJLDRANHEL	416
QY	395	GLIYIMD'IVHSHASNTDGLNMDGJDGHYFHSGRPGHHMMDSRL'FNGNSVEVLEJFL	454
Db	417	GLIYIMD'IVHSHSNTDGLNMDGJDGHYFHSGRGCIHMMDSRL'FNGNSVEVLEJXLL	476
QY	455	SNARKWMLDEYKFDGFRDPGVTSMKTYTHHGLQVDTGYNTEFYATVDVAVY'IMLNDM	514
Db	477	SNARKWMLDEYKFDGFRGVTSMKTYTHHGLQVSTGNTSEYFGATIDYEAVY'IMLNVDL	536
QY	515	IHGJLPEAVYITGEDVSGMPTVCIPVEDGSGVFDYRLHMAVADKWELLIOKRD'DMKMGDI	574
Db	537	IHGJLPEAVYSIGEDVSGMPTFCLPTODGCIAPNRYRLHMAVADKWELLILKOD'DMRGDI	596
QY	575	VAMLNLRNMLEKCVSAYASHQOALVGDITJAFWMLDKMDYFMA'LDLBRSPYL'DRGVALH	634
Db	597	VATLNRNMLEKCVYAYASHQOALVGDITJLAFWMLDKMDYFMA'LDLBRSPYL'DRGJALH	656
QY	635	KHIRTITINGIGEGEGLNMGNEFGHPERJIDP'ROGLHJPSKCFAPGANNYSYD'CORRFFDL	694
Db	657	KHIRTITINGIGEGEGLNMGNEFGHPERJIDP'ROGBHJPNKGIYVGNANNYSYD'CORRFFDL	716
QY	695	GNSKRLR'YHGOERQOALOHLEAAYGEMTSSHOYISRDEDEDRITIEFRGLV'VEVNFHM	754
Db	717	GADLRLR'YHGOERQOALOHLEBERGEMTSSHOYISRKNEDDRYIIFERONLV'VEVNFHM	776
QY	755	TSSYSYD'RYVGLCKPCKYKIVLDSDDPLFGGGRGLSHDAENFSFGCWTDNRP'RMNYTPC	814
Db	777	TNSYSYD'RYVGLCKPCKYKIVLDSDDTLFGGGRNLNHTAEYTSSEGMTDDDRK'SFLVAPFS	836
QY	815	RTAVVYALVEDEVEENE 830	
Db	837	RTAVVYALA-DOGESE 851	

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RESULT 3
ID 042531 PRELIMINARY; PRT; 800 AA.
AC 042531;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, last annotation update)
DE STARCH BRANCHING ENZYME CLASS II (EC 2.4.1.18) (1,4-ALPHA-GLUCAN
DE BRANCHING ENZYME) (GLYCOGEN BRANCHING ENZYME) (AMYLO-(1,4 TO
DE 1,6) TRANSGLUCOSIDASE) (AMYLO-(1,4-1,6)-TRANSGLUCOSYLASE) (FRAGMENT).
DE SBE1 OR SBE2-2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ECOTYPE COLUMBIA; TISSUE=HYPOCOTYL;
RX MEDLINE=96197401; PubMed=8616246;
RA Fisher D.K., Gao M., Kim K.N., Boyer C.D., Gullinan M.J.;
RT "Two closely related cDNAs encoding starch branching enzyme from
RT Arabidopsis thaliana."
RL Plant Mol. Biol. 30:97-108(1996).
CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF
CC GLYCOGEN.
DR EMBL: U22428; AAB03100.1; -;
DR Mendel; 16401; Arabid; Sbe1; 16401.
DR InterPro: IPR000461; -;
DR Pfam: PF00128; alpha-amyase; 1.
FT Transferrase; Glycosyltransferase.
FT NON_TER 1
SQ SEQUENCE 800 AA; 92098 MW; 8D47E9404B403258 CRC64;

Query Match 74.5%; Score 3384.5; DB 10; Length 800;
Best Local Similarity 75.5%; Pred. No. 2.3e-244;
Matches 619; Conservative 80; Mismatches 86; Indels 35; Gaps 8;

QY 12 PCAPLCKSGSTGHHYRTSSCLSFNFK-AFSRRVSGSKSHESDSNVMTASKRYLP 70
DB 11 PSRPL-----NTGFNA--GNSLSEFFKHPKPLSKIFAKQSAEPDSSQAISAEKVL- 62
QY 71 DGRLECYSSSTQDLAPGVYSEE-----SOVLVDESLIMDKIYEDVKNESVPMRETVS 126
DB 63 -----VPDNLDDPPRGFSQIF-DLESQYME---YTEAVRTEDQYTMN---V 100
QY 127 IRRIGSKPRSTIPPGRGORIYDIPSLTGFROHLDYRYSQYKRLREEDIDKESGLDAFSR 186
DB 101 VKERGVKPRIVPPGDKKIYEIDPMLRTYNNHLDYRQYKRLREEDIDKESGLDAFSR 160
QY 187 GYKRGFSSESGITRYRENAFGATMAALIGDPNNMNPADVMTONEGCVWEIFLPNNADG 246
DB 161 GYEKLGFSRSDAGITRYRENAFGAKAASLIGDPNNMNSNADIMTRNFGVWEIFLPNNADG 220
QY 247 SPPIPGSRVVKIRMDTPSGNKSIPAWIKFSYQAPGELPYNGIYDPEEEKYVFKNRP 306
DB 221 SPPIPGSRVVKIRMDTPSGNKSIPAWIKFSYQAPGELPYNGIYDPEEEKYVFKNRP 280
QY 307 KKRKSLRIEIVAGMSSTEPVINTYANFRDVLPRIKRLGYNAVQALMAIQESHYASFGY 366
DB 281 KKRKSLRIEIVAGMSSTEPVINTYANFRDVLPRIKRLGYNAVQALMAIQESHYASFGY 340
QY 367 HTYNFPAASRGTPDDDKSLIDRAHEHGLIYVMDIVYASHASTNTLDGLNFCSTDGHYF 426
DB 341 HTYNFPAASRGTPDDDKSLIDRAHEHGLIYVMDIVYASHASTNTLDGLNFCSTDGHYF 400
QY 427 HSGPRGHMMMDSRLENTGSEVLEFLSLNARWMLDEKFKFGFPEDGTSMMYTHHGLQY 486
DB 401 HSGPRGHMMMDSRLENTGSEVLEFLSLNARWMLDEKFKFGFPEDGTSMMYTHHGLQY 460
QY 487 DPTGNVNEFGIATYDVAVYVLMILNDMTHGLFPRAVITIGDVGSMPTVCIPEEDGGVGF 546

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DB 461 GFTGNVTEYFGLIEDVDVAVNTIYMLVNMKIHGLYEAALITVGEDVSGMFTFCIPVDDGGVGF 520
QY 547 DYRLHMAVADKWEIIOQRDEDMKMGDIYVHMLTNRRLKRCVSYAESHDQALVGDKTIAF 606
DB 521 DYRLHMAVADKWEIIOQRDEDMKMGDIYVHMLTNRRLKRCVSYAESHDQALVGDKTIAF 580
QY 607 WLMQDMYDFAVADKWEIIOQRDEDMKMGDIYVHMLTNRRLKRCVSYAESHDQALVGDKTIAF 666
DB 581 WLMQDMYDFAVADKWEIIOQRDEDMKMGDIYVHMLTNRRLKRCVSYAESHDQALVGDKTIAF 640
QY 667 RGDHLEPGKFEVPGNNYSYDCKRRRFDLGNKHLRYGMOEFOALQHEAVGFMFTSEH 726
DB 641 RGEORLSDGVSITPGNNYSYDCKRRRFDLGNKHLRYGMOEFOALQHEAVGFMFTSEH 700
QY 727 QYISRKDEADRVIVFEGNDLVFENFHWISSYSYDVRGCLPKPKYKIVLSDDPLEFGGFG 786
DB 701 QYISRKDEADRVIVFEGNDLVFENFHWISSYSYDVRGCLPKPKYKIVLSDDPLEFGGFG 760
QY 787 RLSDHAEHSPFEGWYDNRPSFMYTPCRAVYVYALVEDE 826
DB 761 RLSDHAEHSPFEGWYDNRPSFMYTPCRAVYVYALVEDE 800

RESULT 4
ID 09LZS3 PRELIMINARY; PRT; 805 AA.
AC 09LZS3;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, last annotation update)
DE 1,4-ALPHA-GLUCAN BRANCHING ENZYME PROTEIN SOFORM SBE2.2 PRECURSOR.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W., Rudd S.,
RA Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Arabidopsis sequencing project.
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL162506; CAB82930.1; -;
SQ SEQUENCE 805 AA; 92591 MW; 7CE130BD9C4941D0 CRC64;

Query Match 74.5%; Score 3384.5; DB 10; Length 805;
Best Local Similarity 75.5%; Pred. No. 2.3e-244;
Matches 619; Conservative 80; Mismatches 86; Indels 35; Gaps 8;

QY 12 PCAPLCKSGSTGHHYRTSSCLSFNFK-AFSRRVSGSKSHESDSNVMTASKRYLP 70
DB 16 PSRPL-----NTGFNA--GNSLSEFFKHPKPLSKIFAKQSAEPDSSQAISAEKVL- 67
QY 71 DGRLECYSSSTQDLAPGVYSEE-----SOVLVDESLIMDKIYEDVKNESVPMRETVS 126
DB 68 -----VPDNLDDPPRGFSQIF-DLESQYME---YTEAVRTEDQYTMN---V 105
QY 127 IRRIGSKPRSTIPPGRGORIYDIPSLTGFROHLDYRYSQYKRLREEDIDKESGLDAFSR 186
DB 106 VKERGVKPRIVPPGDKKIYEIDPMLRTYNNHLDYRQYKRLREEDIDKESGLDAFSR 165
QY 187 GYKRGFSSESGITRYRENAFGATMAALIGDPNNMNPADVMTONEGCVWEIFLPNNADG 246
DB 166 GYEKLGFSRSDAGITRYRENAFGAKAASLIGDPNNMNSNADIMTRNFGVWEIFLPNNADG 225
QY 247 SPPIPGSRVVKIRMDTPSGNKSIPAWIKFSYQAPGELPYNGIYDPEEEKYVFKNRP 306
DB 221 SPPIPGSRVVKIRMDTPSGNKSIPAWIKFSYQAPGELPYNGIYDPEEEKYVFKNRP 280

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Tue Aug 7 20:32:53 2001

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Page 4

Db 226 SPATPHGSRVIRMDTPSGIKDISIPAMIKFSVOAPGEPINGIYDPEEKEKYVFKHOP 285  
OY 307 KRPSLRIRYSEHVMSSTEVINTYANFRDVLPRIRIKIGYNAVOLMAIOEHSYVASEG 366  
Db 286 KRPSLRIRYSEHVMSSTEVINTYANFRDVLPRIRIKIGYNAVOLMAIOEHSYVASEG 345  
OY 367 HTNRYAASSRFGPDOLSKSLIDRAHEGLVLMYDIYHSASTNTLDGLMFDGTGHTF 426  
Db 346 HTNRYAASSRFGPDOLSKSLIDRAHEGLVLMYDIYHSASTNTLDGLMFDGTGHTF 405  
OY 427 HSGPRGHMMDSRLFNYSWVEVRLFLSNARWMLDEKDFGRFDGVTSMYTHHGLV 486  
Db 406 HSGPRGHMMDSRLFNYSWVEVRLFLSNARWMLDEKDFGRFDGVTSMYTHHGLV 465  
OY 487 DETGYNYEFGYATPDVAVVYLMYLMNDMIGLPEAVTIGEDVSGMPTVCIPVEDGSGVF 546  
Db 466 DETGYNYEFGYATPDVAVVYLMYLMNDMIGLPEAVTIGEDVSGMPTVCIPVEDGSGVF 525  
OY 547 DYRLHNAVADKVEIIOKRDMDKMGDIYHMLTNRNMLEKCVSAESHDOLVADKTI 606  
Db 526 DYRLHNAVADKVEIIOKRDMDKMGDIYHMLTNRNMLEKCVSAESHDOLVADKTI 585  
OY 607 WLMKDMYDPMALDPSPTLIDRGVALHMKMRLITMGIGSGYINFGNNGEHPEDIDP 666  
Db 586 WLMKDMYDPMALDPSPTLIDRGVALHMKMRLITMGIGSGYINFGNNGEHPEDIDP 645  
OY 667 RGDJLHPSKPYPGNNYSYDKRREDGNSKHLRYHGMDFDOLIOHLEAVGFMSTSEH 726  
Db 646 RGDJLHPSKPYPGNNYSYDKRREDGNSKHLRYHGMDFDOLIOHLEAVGFMSTSEH 705  
OY 727 OYTSRDERDRIIVYERKLVYVFNPHMTSSSDYRVCGLRGKXYIYLDSDDDLFGSG 786  
Db 706 OYTSRDERDRIIVYERKLVYVFNPHMTSSSDYRVCGLRGKXYIYLDSDDDLFGSG 765  
OY 787 RLSHDAHFSFEGWYDNRPSFNVYTPCRRATVAVYALVEDE 826  
Db 766 RLSHDAHFSFEGWYDNRPSFNVYTPCRRATVAVYALVEDE 805  
RESULT 5  
OYXGAG PRELIMINARY: PRT: 878 AA.  
ID OYXGAG: PRELIMINARY: PRT: 878 AA.  
AC OYXGAG: PRELIMINARY: PRT: 878 AA.  
DT 01-NOV-1999 (Tremblrel. 12, Created)  
DT 01-NOV-1999 (Tremblrel. 12, last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)  
DE STARCH BRANCHING ENZYME II PRECURSOR (EC 2.4.1.18).  
SBE II.  
OS Solanum tuberosum (Potato).  
OC Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta:  
OC Magnoliophyta: eudicotyledons: core eudicots: Asteridae: euasterids I;  
OC Solanales: Solanaceae: Solanum.  
OX NCBI\_TaxID=4113;  
RN SEQUENCE FROM N.A.  
RC STRAIN=CY. DESIRE.  
RA Jodeling S.A., Schwall G.P., Westcott R.J., Sidebottom C.M., Debet M.,  
Gidley M.J., Jelicic R., Safford R.,  
"A minor form of starch branching enzyme in potato (Solanum tuberosum  
L.) tubers has a major effect on starch structure: cloning and  
RT characterisation of multiple forms of SBE II."  
RL Submitted (Oct-1998) to the EMBL/GenBank/DBD databases.  
DR EMBL: AJ011888; CAB40746.1; -.  
DR InterPro: IPR000461; -.  
DR Pfam: PF00128; alpha-amylase; 1.  
DR Transit peptide; Transferase; Glycosyltransferase.  
FT TRANSIT 1 48 POTENTIAL.  
FT CHAIN 49 878 STARCH BRANCHING ENZYME II.  
SQ SEQUENCE 878 AA: 100411 MW: 558186A39DF8F53 CRC64:  
Query Match 74.4%; Score 3381.5; DB 10; Length 878;  
Best Local Similarity 71.4%; Pred. No. 4.5e-244;

Matches 617; Conservative 95; Mismatches 117; Indels 35; Gaps 5;  
OY 4 YTGSGIFPPCAP-LCKSQSTGFHGYRTSCLSFNFKKAEFRVSGKSSHSISNNVY 62  
Db 3 YTGSGIFPPCAP-LCKSQSTGFHGYRTSCLSFNFKKAEFRVSGKSSHSISNNVY 62  
OY 63 TASKRVYDGC-RICCVSSDOLLEAPCTVSESOVLVDESLMD- - - - -KIVDEV- - - 114  
Db 63 TASKRVYDGC-RICCVSSDOLLEAPCTVSESOVLVDESLMD- - - - -KIVDEV- - - 114  
OY 63 AASKVLPVIGQSSSSSSSDIDPEFAETSPENSPASDVSSMEHSAOIKTEHNDVPS 122  
Db 63 AASKVLPVIGQSSSSSSSDIDPEFAETSPENSPASDVSSMEHSAOIKTEHNDVPS 122  
OY 115 - - - - -NKSVMRETVSIRKGS- - - - -KPSIIPPGRCGRID 148  
Db 123 SDLGVSVELDFPASTLOQEGKLEESKTLNTESEPTIDESDRIRRRGIPPCGCKIYE 182  
OY 149 IDPSLTGFRHLDYRISQYKRLREIDYEGSLDAPSRGYEKGRSFTGTYREMAFG 208  
Db 183 IDPSLTGFRHLDYRISQYKRLREIDYEGSLDAPSRGYEKGRSFTGTYREMAFG 242  
OY 209 ATWALLIDFNNMNPADVMTQNCQWELFIPNADGSPPIPHSGSVKTRMDTPSGND 268  
Db 243 AOSAAALIDFNNMNPADVMTQNCQWELFIPNADGSPPIPHSGSVKTRMDTPSGND 302  
OY 269 SIPAMIKFSVOAPGELPYNGIYDPEEKEKYVFNPKRPSLRIRYSEHVMSSTEVY 328  
Db 303 SIPAMIKFSVOAPGELPYNGIYDPEEKEKYVFNPKRPSLRIRYSEHVMSSTEVY 362  
OY 329 NTYANFRDVLPRIRIKIGYNAVOLMAIOEHSYVASEGHTYNTNYAASSRFGPDOLSKSL 388  
Db 363 NTYANFRDVLPRIRIKIGYNAVOLMAIOEHSYVASEGHTYNTNYAASSRFGPDOLSKSL 422  
OY 389 DRAHEGLVLMYDIYHSASTNTLDGLMFDGTGHTFHSRGRHMMDSRLFNYSWVE 448  
Db 422 DRAHEGLVLMYDIYHSASTNTLDGLMFDGTGHTFHSRGRHMMDSRLFNYSWVE 482  
OY 449 VRLFLSNARWMLDEKDFGRFDGVTSMYTHHGLVDTGNTNEXFGATVDAVYVL 508  
Db 483 VRLFLSNARWMLDEKDFGRFDGVTSMYTHHGLVDTGNTNEXFGATVDAVYVL 542  
OY 509 MLLNDMIGLPEAVTIGEDVSGMPTVCIPVEDGSGVGFYRLHNAVADKVEIIOKRD 568  
Db 543 MLLNDMIGLPEAVTIGEDVSGMPTVCIPVEDGSGVGFYRLHNAVADKVEIIOKRD 602  
OY 569 WKMGDIYHMLTNRNMLEKCVSAESHDOLVADKTIAMLMKDMYDPMALDPSPTLID 628  
Db 603 WKMGDIYHMLTNRNMLEKCVSAESHDOLVADKTIAMLMKDMYDPMALDPSPTLID 662  
OY 629 RGVATLHMLTNRNMLEKCVSAESHDOLVADKTIAMLMKDMYDPMALDPSPTLID 688  
Db 663 RGVATLHMLTNRNMLEKCVSAESHDOLVADKTIAMLMKDMYDPMALDPSPTLID 722  
OY 689 RRRFDLNSKHLRYHGMDFDOLIOHLEAVGFMSTSEHOYTSRDERDRIIVYERKLV 748  
Db 723 RRRFDLNSKHLRYHGMDFDOLIOHLEAVGFMSTSEHOYTSRDERDRIIVYERKLV 782  
OY 749 VFNHMTSSYDTRVGLKRGKXYIYLDSDDDLFGSGRRLSHDAHFSFEGWYDNRPSF 808  
Db 783 VFNHMTSSYDTRVGLKRGKXYIYLDSDDDLFGSGRRLSHDAHFSFEGWYDNRPSF 842  
OY 809 MYTTPCCTAVVAVYALVEDEVEELE 832  
Db 843 MYTTPCCTAVVAVYALVEDEVEELE 866  
RESULT 6  
ID OYXGAG: PRELIMINARY: PRT: 858 AA.  
AC OYXGAG: PRELIMINARY: PRT: 858 AA.  
DT 01-JUN-1998 (Tremblrel. 05, Created)  
DT 01-JUN-1998 (Tremblrel. 05, last sequence update)  
DT 01-MAY-2000 (Tremblrel. 13, last annotation update)  
DE STARCH BRANCHING ENZYME II (EC 2.4.1.18) (1,4-ALPHA-GLUCAN BRANCHING  
ENZYME) (GLYCOSYL TRANSFERASE) (AMYLO- (1,4-1,6)-TRANSGLUCOSYLASE).  
DE 1,6) TRANSGLUCOSYLASE) (AMYLO- (1,4-1,6)-TRANSGLUCOSYLASE).



GN SBE1 OR SBE2.1 OR F1011.2.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids II;  
 OC Brassicales; Brassicaceae; Arabidopsis.  
 RX NCBI\_TaxID=3702;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV, COLUMBIA;  
 RA Khoshnood J.;  
 RL Thesis (1997), Swedish University of Agricultural Sciences, Sweden.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV, COLUMBIA;  
 RA Lin X., Kaul S., Sneha T.P., Fujii C.Y., Shen M., Vanaken S.E.,  
 RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.,  
 RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,  
 RA Fraser C.M., Venter J.C.;  
 RT "Arabidopsis thaliana chromosome II BAC F1011 genomic sequence,"  
 RT Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF  
 CC GLUCOGEN.  
 DR EMBL: AJ000497; CAA04134.1; -  
 DR EMBL: AC006919; AAD24644.1; -  
 DR Mendel: 24099; Arabidopsis:24099.  
 DR InterPro: IPR000461; -  
 DR Pfam: Pf00128; alpha-amylase; 1.  
 DR Transferrase: Glycosyltransferase.  
 KW SEQUENCE 858 AA; 97659 MW; E1D61C0C21D456F1 CRC64;  
 SQ  
 Query Match 74.2%; Score 3373; DB 10; Length 858;  
 Best Local Similarity 72.0%; Pred. No. 1.9e-243;  
 Matches 617; Conservative 104; Mismatches 102; Indels 34; Gaps 6;  
 QY 4 YTTGIRPCAPLCKSOSTGFGYR--RTSCLSFKE--AFSRRVSGKSHESDSS 58  
 DB 3 YTTGIRPCAPLCKSOSTGFGYR--RTSCLSFKE--AFSRRVSGKSHESDSS 62  
 QY 59 NMYATKARVLPDRICYSSTDLQLEAPGVSESOVLTVESLIMDKIYDEVENKS 118  
 DB 63 SLATTYASER-LRHHOSDSSASDQVOSRDYVSDDTQVGLGNDV-----VQKTEAGDT 114  
 QY 119 VPMREYSIRKIGS-----KPSIRPGRGORITDPSLTFRQHL 160  
 DB 115 EPTDQTSALSTSGISYKEDFAKMSHVQEVQGRKIPPGGGRKTYDIPMLNSHRHL 174  
 QY 161 DYRSQYKRLREIDYEGSLDFAFSRGYKFGFSRSETGITREMAPGATMALIGDPNN 220  
 DB 175 DYRGQYKRLREIDYEGSLDFAFSRGYKFGFSRSETGITREMAPGATMALIGDPNN 234  
 QY 221 WPNADVMTQNEGVWEITLPPNADGSPRIPHSRRTKIMDTPSGNKSIPAMIKESVOA 280  
 DB 235 WNAKSDVMAINDGVWEITLPPNADGSPRIPHSRRTKIMDTPSGNKSIPAMIKESVOA 294  
 QY 281 PGEIPLNGIYDPEEEKYVFNKPKRSLRIYESHVGSSTPVIINTANFRDVL 340  
 DB 295 PGEIPLNGIYDPEEEKYVFNKPKRSLRIYESHVGSSTPVIINTANFRDVL 354  
 QY 341 RIKKLGYNVQALMAIOEHSYVAFGYHVTNFAAASRFGTDDKSLIDKAHELGLVL 400  
 DB 355 RIKKLGYNVQALMAIOEHSYVAFGYHVTNFAAASRFGTDDKSLIDKAHELGLVL 414  
 QY 401 DIYHSHASTNTDGLMFGTGDGHYFHSGPRGHMMMSRLFNYSWVLEFLLSNARW 460  
 DB 415 DIYHSHASTNTDGLMFGTGDGHYFHSGPRGHMMMSRLFNYSWVLEFLLSNARW 474  
 QY 461 LDEYKDFGRFDGVTSMATYHGLQVDFGNNEFGYATVDVAVYUMLINDMIGLEP 520  
 DB 475 LDEYKDFGRFDGVTSMATYHGLQVDFGNNEFGYATVDVAVYUMLINDMIGLEP 534  
 QY 521 EANTIGEDSVMPYICIPEDGCVFDRILAAVADKVEITIKRDEDMKGDIVHMLTN 580  
 DB 581 EANTIGEDSVMPYICIPEDGCVFDRILAAVADKVEITIKRDEDMKGDIVHMLTN 594

DB 535 EALVGEDVSGMPCARVPEDEGVGFYRLHMAVADKMIELKKRDEDMOYDITTLN 594  
 QY 581 RHWLCKCYAESHDQALVSKTIAFWLMDKMDYFMAIDRPPSTPLIDRGVALHKMIRL 640  
 DB 595 RHWLCKCYAESHDQALVSKTIAFWLMDKMDYFMAIDRPPSTPLIDRGVALHKMIRL 654  
 QY 641 TWGLGEGYLNPMGNENEPHGPIDPGLDLPISGKRVPPNNNSYDKCRREFLGSKHL 700  
 DB 655 TWGLGEGYLNPMGNENEPHGPIDPGLDLPISGKRVPPNNNSYDKCRREFLGSKHL 714  
 QY 701 RYHGMQEPDQALHLEAVYGFMTSEHGYISRKDERRIYFERNGLVFNFMHTSSYS 760  
 DB 715 RYHGMQEPDQALHLEAVYGFMTSEHGYISRKDERRIYFERNGLVFNFMHTSSYS 774  
 QY 761 YRVCGLKRGKTYLDSDPLFGFGLSHDAHFSEGYDNRPSEVYTPCRAVY 820  
 DB 775 YRVCGLKRGKTYLDSDPLFGFGLSHDAHFSEGYDNRPSEVYTPCRAVY 834  
 QY 821 ALVDEVEENE--LEPV 834  
 DB 835 AAVDDDDDDERSLVP 851  
 RESULT 7  
 ID 09XGA5 PRELIMINARY; PRT; 871 AA.  
 AC 09XGA5;  
 DT 01-NOV-1999 (TREMURel. 12, Created)  
 DT 01-NOV-1999 (TREMURel. 12, Last sequence update)  
 DT 01-MAR-2001 (TREMURel. 16, Last annotation update)  
 DE STARCH BRANCHING ENZYME II PRECURSOR (EC 2.4.1.18).  
 GN SBE II.  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;  
 OC Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV, DESIREE;  
 RA Jobling S.A., Schwall G.P., Westcott R.J., Sidebottom C.M., Debet M.,  
 RA Gidley M.J., Jeffcoat R., Safford R.;  
 RT "A minor form of starch branching enzyme in potato (Solanum tuberosum  
 RT L.) tubers has a major effect on starch structure; cloning and  
 RT characterisation of multiple forms of SBE II.";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ011885; CAB40743.1; -  
 DR InterPro: IPR000461; -  
 DR Pfam: Pf00128; alpha-amylase; 1.  
 KW Transferrase: Glycosyltransferase.  
 FT TRANSIT 1 48 POTENTIAL.  
 FT CHAIN 49 871 STARCH BRANCHING ENZYME II.  
 SQ SEQUENCE 871 AA; 99417 MW; 6F1F094247676938 CRC64;  
 Query Match 73.9%; Score 3360; DB 10; Length 871;  
 Best Local Similarity 71.4%; Pred. No. 1.8e-242;  
 Matches 619; Conservative 94; Mismatches 118; Indels 36; Gaps 6;  
 QY 4 YTTGIRPCAP-LCKSOSTGFGYRRTSSCLSFKEAFSRVSGKSHESDSSNMY 62  
 DB 3 YTTGIRPCAP-LCKSOSTGFGYRRTSSCLSFKEAFSRVSGKSHESDSSNMY 62  
 QY 63 TASKRVL-PDGRICYSSTDLQLEAPGVSESOVLTVESLIMD-----RIVEDEV--- 114  
 DB 63 AASGKYLAVGCTSDSSSSSTDFEFTETSPENSPASTVDSYHEHSAQITTEMDDVPS 122  
 QY 115 -----KESVPMREYSIRKIGS-----KPSIRPGRGORITD 148  
 DB 123 SDLTGSVEFLDASSLQIQEGGKLEESKTLNTPSETIILDESDRIRERGIPIPGIGQIYE 182  
 QY 149 IDPSLTGFRQHLQDYRSQYKRLREIDYEGSLDFAFSRGYKFGFSRSETGITREMAPG 208  
 DB 208 IDPSLTGFRQHLQDYRSQYKRLREIDYEGSLDFAFSRGYKFGFSRSETGITREMAPG 212

Db 183 IDPLLTNYKOHLDYRYSOYKRLREAIIDRYEGGLEAFSGYKMGFTSANTGITYREMAPG 242  
 OY 209 ATWAAALIDGFNNMNPADWMTQNECGWVEIFLPPNADGSPPIPHGSRVYKIRMDTPSGNKD 268  
 Db 243 AQSALLIDGFNNMNPADWMTQNECGWVEIFLPPNADGSPPIPHGSRVYKIRMDTPSGNKD 302  
 OY 269 STPAMKESVOAPGELPYNIGIYDPEEKEKYKFNOPRKRKSLRTIYSHVMSSTPEVI 328  
 Db 303 STPAMKESVOAPGELPYNIGIYDPEEKEKYKFNOPRKRKSLRTIYSHVMSSTPEVI 362  
 OY 329 NTYANFRDVLPRIRIKLGNAYOLMAIOHSHYASFGHYVTFEYVAASSFGPTDPLKSI 388  
 Db 363 NSTVNRDVLPRIRIKLGNAYOLMAIOHSHYASFGHYVTFEYVAASSFGPTDPLKSI 422  
 OY 389 DKAHELGLVLMIDYVSHASTYTLGLNPFDOGTGHIYHSGRGHHMMWDSRLFYGSME 448  
 Db 423 DKAHELGLVLMIDYVSHASTYTLGLNPFDOGTGHIYHSGRGHHMMWDSRLFYGSME 482  
 OY 449 VLRFLLSNARWMLDEYKFGDFRFGVTSMTYTHHGLQVDFGNTNNEYGYATDVAVYL 508  
 Db 483 VLRFLLSNARWMLDEYKFGDFRFGVTSMTYTHHGLQVDFGNTNNEYGYATDVAVYL 542  
 OY 509 MLNDMHLGLFPEAVYIGEDVSGMPTVCIPVEDGSGVGFYRLHMAVADKWEIIOKRED 568  
 Db 543 MLNDMHLGLFPEAVYIGEDVSGMPTVCIPVEDGSGVGFYRLHMAVADKWEIIOKRED 602  
 OY 569 WKMGDIYVHMLTNRMWLEKCVSAESHDQALVGDKTAFWLMMDKMDYDFMALDRPSTPLID 628  
 Db 603 WKMGDIYVHMLTNRMWLEKCVSAESHDQALVGDKTAFWLMMDKMDYDFMALDRPSTPLID 662  
 OY 629 RGVALHKMRLTLMGAGGEGYTLNFMNGERGHPEWIDFPGDHLPSGKVPNGNYSYDKC 688  
 Db 663 RGVALHKMRLTLMGAGGEGYTLNFMNGERGHPEWIDFPGDHLPSGKVPNGNYSYDKC 722  
 OY 689 RRRFDLGNKHLRYHGMOFDOALQHLERAYGFMSEHGYISRKDRDRITVERGNLYF 748  
 Db 723 RRRFDLGNKHLRYHGMOFDOALQHLERAYGFMSEHGYISRKDRDRITVERGNLYF 782  
 OY 749 VFNFMHTSSYSDYRVGCLKPKKRYIVLSDPLFGGFGRLSHDAHEFSPGAWDNPRSF 808  
 Db 783 VFNFMHTSSYSDYRVGCLKPKKRYIVLSDPLFGGFGRLSHDAHEFSPGAWDNPRSF 842  
 OY 809 MYVTPCRTAVVYALVLED-EYENLEPVA 834  
 Db 843 MYVTPCRTAVVYALVLED-EYENLEPVA 869

RESULT 8  
 OXGAB PRELIMINARY; PRT; 882 AA.  
 AC OXGAB;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE STARCH BRANCHING ENZYME II PRECURSOR (EC 2.4.1.18).  
 SBE II.  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta;  
 OC Magnoliophyta: eudicotyledons: core eudicots: Asteridae: euasterids I;  
 OC Solanales: Solanaceae: Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV DESIREE;  
 RA JODLING S.A., Schwab, G.P., Westcott R.J., Sidebottom C.M., Debet M.,  
 "A minor form of starch branching enzyme in potato (Solanum tuberosum  
 L.) tubers has a major effect on starch structure: cloning and  
 characterisation of multiple forms of SBE II.",  
 RL Submitted (Oct-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AJ011890; CAB40748.1; -  
 DR InterPro: IPR000461; -  
 DR Pfam: PF00128; alpha-amylase; 1.

KW Transf. peptide; Transferrase; Glycosyltransferase.  
 FT TRANSIT 49 882 POTENTIAL.  
 FT CHAIN 48 STARCH BRANCHING ENZYME II.  
 SO SEQUENCE 882 AA; 100863 MW; F850F9AF825EB87 CRC64;

Query Match 73.8%; Score 3356; DB 10; Length 882;  
 Best Local Similarity 70.9%; Pred. No. 3.6e-242;  
 Matches 617; Conservative 96; Mismatches 119; Indels 38; Gaps 6;

OY 4 YTGIRFPCAP-LCKSQSTGFHGYRTSSCLSPNFKAPSRVYFGSKSHESDSSNMY 62  
 Db 3 YTLGSEVFPYVPSYKNGFSSNGDRNNAVSVFLKHSLSRKILKESYSNIFRPSTV 62  
 OY 63 TASKRVL-PDGRTECYSSSTDOLEAPCTVSESOVLTVESLMD--KIVZDEY--- 114  
 Db 63 AASGKVLVPGTQSDSSSSSTDOLEAPCTVSESOVLTVESLMD--KIVZDEY--- 122  
 OY 115 ---NKSVPMTRETVSIRKIGS-----KPSLPPG RGQRITD 148  
 Db 123 SDLGVSVEIDFASSLDQEGCKLEESKTLNTSPETIIDESDRIRERGIPEGLQIYE 182  
 OY 149 IDPLTGRHOLDYRYSOYKRLREAIIDRYEGGLEAFSGYKMGFTSANTGITYREMAPG 208  
 Db 183 IDPLTGRHOLDYRYSOYKRLREAIIDRYEGGLEAFSGYKMGFTSANTGITYREMAPG 242  
 OY 209 ATWAAALIDGFNNMNPADWMTQNECGWVEIFLPPNADGSPPIPHGSRVYKIRMDTPSGNKD 268  
 Db 243 AQSALLIDGFNNMNPADWMTQNECGWVEIFLPPNADGSPPIPHGSRVYKIRMDTPSGNKD 302  
 OY 269 STPAMKESVOAPGELPYNIGIYDPEEKEKYKFNOPRKRKSLRTIYSHVMSSTPEVI 328  
 Db 303 STPAMKESVOAPGELPYNIGIYDPEEKEKYKFNOPRKRKSLRTIYSHVMSSTPEVI 362  
 OY 329 NTYANFRDVLPRIRIKLGNAYOLMAIOHSHYASFGHYVTFEYVAASSFGPTDPLKSI 388  
 Db 363 NSTVNRDVLPRIRIKLGNAYOLMAIOHSHYASFGHYVTFEYVAASSFGPTDPLKSI 422  
 OY 389 DKAHELGLVLMIDYVSHASTYTLGLNPFDOGTGHIYHSGRGHHMMWDSRLFYGSME 448  
 Db 423 DKAHELGLVLMIDYVSHASTYTLGLNPFDOGTGHIYHSGRGHHMMWDSRLFYGSME 482  
 OY 449 VLRFLLSNARWMLDEYKFGDFRFGVTSMTYTHHGLQVDFGNTNNEYGYATDVAVYL 508  
 Db 483 VLRFLLSNARWMLDEYKFGDFRFGVTSMTYTHHGLQVDFGNTNNEYGYATDVAVYL 542  
 OY 509 MLNDMHLGLFPEAVYIGEDVSGMPTVCIPVEDGSGVGFYRLHMAVADKWEIIOKRED 568  
 Db 543 MLNDMHLGLFPEAVYIGEDVSGMPTVCIPVEDGSGVGFYRLHMAVADKWEIIOKRED 602  
 OY 569 WKMGDIYVHMLTNRMWLEKCVSAESHDQALVGDKTAFWLMMDKMDYDFMALDRPSTPLID 628  
 Db 603 WKMGDIYVHMLTNRMWLEKCVSAESHDQALVGDKTAFWLMMDKMDYDFMALDRPSTPLID 662  
 OY 629 RRRFDLGNKHLRYHGMOFDOALQHLERAYGFMSEHGYISRKDRDRITVERGNLYF 748  
 Db 723 RRRFDLGNKHLRYHGMOFDOALQHLERAYGFMSEHGYISRKDRDRITVERGNLYF 782  
 OY 749 VFNFMHTSSYSDYRVGCLKPKKRYIVLSDPLFGGFGRLSHDAHEFSPGAWDNPRSF 808  
 Db 783 VFNFMHTSSYSDYRVGCLKPKKRYIVLSDPLFGGFGRLSHDAHEFSPGAWDNPRSF 842  
 OY 809 MYVTPCRTAVVYALVLED-EYENLEPVA 835  
 Db 843 MYVTPCRTAVVYALVLED-EYENLEPVA 872

RESULT 9  
 OXGAB PRELIMINARY; PRT; 882 AA.  
 AC OXGAB;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE STARCH BRANCHING ENZYME II PRECURSOR (EC 2.4.1.18).  
 SBE II.  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta;  
 OC Magnoliophyta: eudicotyledons: core eudicots: Asteridae: euasterids I;  
 OC Solanales: Solanaceae: Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV DESIREE;  
 RA JODLING S.A., Schwab, G.P., Westcott R.J., Sidebottom C.M., Debet M.,  
 "A minor form of starch branching enzyme in potato (Solanum tuberosum  
 L.) tubers has a major effect on starch structure: cloning and  
 characterisation of multiple forms of SBE II.",  
 RL Submitted (Oct-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AJ011890; CAB40748.1; -  
 DR InterPro: IPR000461; -  
 DR Pfam: PF00128; alpha-amylase; 1.



DB 181 GFTRSATGITYREWAPGASALIDGFNNMMDANADIMTRNEFGWEIFLPNNVDGSPAIP 240  
 QY 252 HGSRAKIMNDPSPGKNSDIPAMIKFSVOAPGELPYNGIYYPPEBEKVFKNPOPKRPS 311  
 DB 241 HGSRAKIMNDPSPGKNSDIPAMINISIQLPDEIPYNGIYYPPEBEKVFKNPOPKRPS 300  
 QY 312 LRIYSHGMSSTEPVITTYANRFDVLPRIKIGYNAVOMALTOEHSYASFGYHTNF 371  
 DB 301 LRIYSHGMSSTEPVITTYANRFDVLPRIKIGYNAVOMALTOEHSYASFGYHTNF 360  
 QY 372 YASASRETPDRIKILDKAHEIGLYVMDIVHSHASTNTDGLMPDGTGCHPESGPR 431  
 DB 361 FAPSRFGIPDOKSLDKAHEIGLYVMDIVHSHASTNTDGLMPDGTGCHPESGPR 420  
 QY 432 GHMMMDRLNENYGSWEYLRELLSNARWMLDEYKFGDPDGVTSMTYTHGLDVFDTGN 491  
 DB 421 GHMMMDRLNENYGSWEYLRELLSNARWMLDEYKFGDPDGVTSMTYTHGLDVFDTGN 480  
 QY 492 YNEEYATDVAVYVYLMNDMLHGLEPEAVTIGEDVSGMPTVCIPVEDGSGVEDYRLH 551  
 DB 481 YNEEYATDVAVYVYLMNDMLHGLEPEAVTIGEDVSGMPTVCIPVEDGSGVEDYRLH 540  
 QY 552 MAVADKWEIIOKRDMDKMDIVHMLNRRWLEKCVSYASHDQALVGDKTIFWIMDK 611  
 DB 541 MAVADKWEIIOKRDMDKMDIVHMLNRRWLEKCVSYASHDQALVGDKTIFWIMDK 600  
 QY 612 DMYDENALDRSTPLIDGVALHMKIRLITGGLGEGYLNMGNEFGHPEDIDPRGDLH 671  
 DB 601 DMYDENALDRSTPLIDGVALHMKIRLITGGLGEGYLNMGNEFGHPEDIDPRGDLH 660  
 QY 672 LPSCFVGNVSYKCRRRFDIGSKRLRYHGMGEFOALOHLEAVGEMTSEHOYTSR 731  
 DB 661 LPSCFVGNVSYKCRRRFDIGSKRLRYHGMGEFOALOHLEAVGEMTSEHOYTSR 720  
 QY 732 KDERRITVFERGNLYVFENFHTSSYSDRYGCLPKGKYKIVLSDPRLTGGRGRLSHD 791  
 DB 721 KDERRITVFERGNLYVFENFHTSSYSDRYGCLPKGKYKIVLSDPRLTGGRGRLSHD 780  
 QY 792 AHEFEGEYDNRPSFENYTPPCRAVYALY--EDVEVENLEPYA 835  
 DB 781 AHEFEGEYDNRPSFENYTPPCRAVYALY--EDVEVENLEPYA 826

RESULT 11  
 ID Q42526 PRELIMINARY; PRT; 854 AA.  
 AC Q42526;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)  
 DE STRACH BRANCHING ENZYME CLASS II (EC 2.4.1.18) (1,4-ALPHA-GLUCAN  
 BRANCHING ENZYME) (GLYCOGEN BRANCHING ENZYME) (AMULO-(1,4 TO  
 1,6)TRANSGLUCOSIDASE) (AMULO-(1,4-1,6)-TRANSGLUCOSYLASE) (FRAGMENT).  
 GN SBEI OR SBE2-1.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Euryotia, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN  
 RP  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA; TISSUE=SEEDLING HYPOCOTYLS;  
 RX MEDLINE=96197401; Pubmed=8616246;  
 RA Fisher D.K., Gao M., Kim K.N., Boyer C.D., Gullithan M.J.,  
 RT "Two closely related cDNAs encoding starch branching enzyme from  
 Arabidopsis thaliana."  
 RL Plant Mol. Biol. 30:97-108(1996).  
 CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF  
 GLYCOGEN.  
 DR EMBL; U18817; AAB0309.1; -;  
 DR Medel; 16400; Arabid; Spel; 16400.  
 DR InterPro; IPR000461; -;  
 DR Pfam; PF00128; alpha-amylase; 1.

KW Transferase; Glycosyltransferase.  
 FT NON\_TER 1  
 SQ SEQUENCE 854 AA; 97229 MW; 6701222ETBD331FC CRC64;  
 Query Match 73.2%; Score 3327; DB 10; Length 354;  
 Best Local Similarity 71.5%; Pred. No. 5, 1e-240;  
 Matches 609; Conservative 105; Mismatches 104; Indels 34; Gaps 6;  
 QY 9 IRPPCAPLCSOSTGPHGR---RTSCLSFENKE--AFSRVFGSGKSSHESQSSNVMT 63  
 DB 4 VRPHPLPSIKKNSLSHFNEDLRSMNVSFLRKRSRSGCFAPKPPSYDSQSSSLNT 63  
 QY 64 ASKRVLPDGRKEICYSSTQLEAPGVSESVYLDVSELMDDKIVEDEKESVPME 123  
 DB 64 ASER-LRGHSDSSSASDQVOSRDVSDTOYLVND-----VQTEEAQETETLDQ 115  
 QY 124 TVSIRKIGS-----KPSIIPPGRGRIYIDPSTLGFQJLDYRS 165  
 DB 116 TSAISTGSIYKEDPAKMSHVDOEGQRKLPPEDGKRITDIDMLNSHRNHDYRG 175  
 QY 166 QYRLREIDRYEGSLDAFSRGYEKEFGFSRSETGITYREMAPGATWALLIGDFNNMNPNA 225  
 DB 176 QYRLREIDRYEGSLDAFSRGYEKEFGFSRSETGITYREMAPGATWALLIGDFNNMNPNA 235  
 QY 226 DVMTONECGWEIFLPNNMADGSPPIPHGSRVKLRMDTPSGNDSIPAWTKFSVOAGELP 285  
 DB 236 DVMTONECGWEIFLPNNMADGSPPIPHGSRVKLRMDTPSGNDSIPAWTKFSVOAGELP 295  
 QY 286 YNGIYDPEEKEKYVFNKNPOPKRPSLRIYESHVSGSTEPYINTYANRFDVLPRIKIL 345  
 DB 296 YNGIYDPEEKEKYVFNKNPOPKRPSLRIYESHVSGSTEPYINTYANRFDVLPRIKIL 355  
 QY 346 GYNAVOMALTOEHSYASFGYHTNFYASSRGCPDDKLSLIDKHEIGLYVMDIYHS 405  
 DB 356 GYNAVOMALTOEHSYASFGYHTNFYASSRGCPDDKLSLIDKHEIGLYVMDIYHS 415  
 QY 406 HASTNTDGLMPDGTGCHPESGPRGHMMMDRLNENYGSWEYLRELLSNARWMLDEYK 465  
 DB 416 HASTNTDGLMPDGTGCHPESGPRGHMMMDRLNENYGSWEYLRELLSNARWMLDEYK 475  
 QY 466 FDGFRDGVTSMTYTHGLQVDTGYNTEPGYADVAVYVYLMNDMLHGLEPEAVTI 525  
 DB 476 FDGFRDGVTSMTYTHGLQVDTGYNTEPGYADVAVYVYLMNDMLHGLEPEAVTI 535  
 QY 526 GEDVSGMPTVCIPVEDGSGVEDYRLHMAVADKWEIIOKRDMDKMDIVHMLNRRWLE 585  
 DB 536 GEDVSGMPTVCIPVEDGSGVEDYRLHMAVADKWEIIOKRDMDKMDIVHMLNRRWLE 595  
 QY 586 KCVSYASHDQALVGDKTIFWIMDKMDYDFMALDRSPPLIDRGVALHMKIRLITMGIG 645  
 DB 596 KCVSYASHDQALVGDKTIFWIMDKMDYDFMALDRSPPLIDRGVALHMKIRLITMGIG 655  
 QY 646 GEGYLNMGNEFGHPEDIDPRGDLHPSGKFEYGNVSYKCRRRFDIGSKRLRYHGM 705  
 DB 656 GEGYLNMGNEFGHPEDIDPRGDLHPSGKFEYGNVSYKCRRRFDIGSKRLRYHGM 715  
 QY 706 QERDOALTOHLEAVGEMTSEHOYTSRDERRTIYERENLYVFENFHTSSYSDRYGVC 765  
 DB 716 QERDOALTOHLEAVGEMTSEHOYTSRDERRTIYERENLYVFENFHTSSYSDRYGVC 775  
 QY 766 LRGKAKYIVLSDPRLTGGRGRLSHDAHSPFGGVDNRPSPMYTTPCORTAVVAVLAD 825  
 DB 776 SVFGKRIYVLDNSLFLGGFNRLDSDSEFFTSGRHDDPCSFMYTTPCORTAVVAVLAD 835  
 QY 826 EVENE--LEPV 834  
 DB 836 DDDERSSLVPI 847

RESULT 12  
 ID Q9SXI9 PRELIMINARY; PRT; 841 AA.  
 Q9SXI9

AC 095X19:  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE STARCH BRANCHING ENZYME RBE4.  
 GN RBE4.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae;  
 OC Oryza.  
 NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Mizuno K., Tachibana M., Kobayashi E., Kawasaki T., Funane K.,  
 RA Kobayashi M., Baba T.,  
 RT "Molecular cloning and expression analysis of a novel member of starch  
 RT branching enzyme isoform in developing rice seeds."  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB023498; BAA82828.1;  
 DR InterPro: IPR000461;  
 DR InterPro: IPR002160;  
 DR Pfam: PF00128; alpha-amylase; 1.  
 DR ProDom; PD000891; 1.  
 DR PRODOM 841 AA; 94779 MW; 9A547A52A6216215 CRC64;  
 SQ

Query Match 72.9%; Score 3315; DB 10; Length 841;  
 Best Local Similarity 74.9%; Pred. No. 3.9e-239;  
 Matches 611; Conservative 66; Mismatches 99; Indels 40; Gaps 6;

36 FNEKFAFSRRVFS-----GK-----SSHESDSNNMTAKRVLPDGRIEYS 78  
 40 FRKROFSRGVYSCAGAPGVLPVGGSDLLSAPVETQEOPEESQIPDDKRVKFE 99  
 79 SSTDLAAGCTYS-----EESQVLTDESILMDKIVEDEYKESVPMRETVSIRK 129  
 100 EE-EELPAVAEASIKVVAEDKLESEVIODIE-----ENVETGVIKADERTVE----- 147  
 130 IGSRSRSTPGRGORIVDIDPSLGFROHLDYRSQKRLREIDKYEGSLAFSGYE 189  
 148 --DKRVRIPPDGDKITQIDPMLGEFNHLDYRSSEKRRRAIDHDEGLDAFSGYE 205  
 190 KGSRSRSTGITYREMAAGATMAALIGDPMNPNADVTONEGWEIFLPPNADGSP 249  
 206 KLGFRSAEGITYREMAAGASALVGFENMNNADTMRNEGVWEISLPNADGSPA 265  
 250 IPHGRVAKIRMDTPSGNNDSPANIKFSVOAGELPYNGIYDPEPEEKYVFPKPKRP 309  
 266 IPHGRVAKIRMDTPSGVNDSPANIKFPAVOAGELPYNGIYDPEPEEKYVFPKPKRP 325  
 310 KSLRTYESHVGMSSTEVINTYANFRDDVLPRIKKIGVNVOLMAIOEHSYASFGYHT 369  
 326 NSLRYESHIGMSPEPKINTYANFRDEVPRIKKIGVNVOLMAIOEHSYASFGYHT 385  
 370 NEYAASSRFGIPDLKSLIDKAEHLGLVLMIDIVHSHASTNTLDGLNMFDDGTGHHFSG 429  
 386 NEYAPSSRFGIPDLKSLIDKAEHLGLVLMIDIVHSHASTNTLDGLNMFDDGTGHHFSG 445  
 430 PRGHMMAMDRLTFNYGSEVLEFLLSNARMMDEYKFDGFRFGVTSMMYTHHGLQVDT 489  
 446 PRGHMMAMDRLTFNYGSEVLEFLLSNARMMDEYKFDGFRFGVTSMMYTHHGLQVDT 505  
 490 GNTRETFGYTVDVAVVYLMIDMTLHGLPEAVTIGEVNSGMPVCPIVEGSGVGFDR 549  
 506 GNTRETFGYTVDVAVVYLMIDMTLHGLPEAVTIGEVNSGMPVCPIVEGSGVGFDR 565  
 550 LHAADVADKVAEIIOKRDEMKDGYTHMLTNRALEKCVSYAESHDQALVGDKTAFWLM 609  
 566 LHAADVADKVAEIIOKRDEMKDGYTHMLTNRALEKCVSYAESHDQALVGDKTAFWLM 625  
 610 DKMTDFMALDRSTPLIDRGVALHMKRLITMGEGEGEYLFNFMENEGHPPMTDFPRGD 669  
 626 DKMTDFMALDRSTPLIDRGVALHMKRLITMGEGEGEYLFNFMENEGHPPMTDFPRGD 685

OY 670 LHLPSGKFPVPGNNYSYDKRRRFDLGNKHLRYHGMQEFQOATOHLEAYGFWTSHOYT 729  
 DB 686 OSLPGSVLPNGNNSPFKCRKRRLPLGADYLRTHGMQEFQOAMHLEAYGFWTSHOYT 745  
 OY 730 SRKBERDRIYFERGNLVFVFNFMHTSSYSYDYRVGCLPKGKYKIVLSDDPLEFGGFRGS 789  
 DB 746 SRKHEEDKVIIFERGDVLFVFNFMHTSSYSYDYRVGCLPKGKYKIVLSDDPLEFGGFRGS 805  
 OY 790 HDAEHFEFGWYDNRPRSPFMYTPPCRTAVYALVED 825  
 DB 806 HDAEHFEFGWYDNRPRSPFMYTPPCRTAVYALVED 841

RESULT 13  
 ID 024421 PRELIMINARY; PRT; 814 AA.  
 AC 024421;  
 DT 01-JAN-1998 (TReMBLrel. 05, Created)  
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)  
 DE STARCH BRANCHING ENZYME IIA (EC 2.4.1.18) (1.4-ALPHA-GLUCAN BRANCHING  
 DE ENZYME) (GLYCOGEN BRANCHING ENZYME) (AMTLO-1.4 TO  
 DE 1,6)TRANSGLUCOSIDASE) (AMTLO-1.4-1.6)-TRANSGLUCOSYLASE) (FRAGMENT).  
 GN SBE1 OR SBE2A.  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae;  
 OC Andropogoneae; Zea.  
 NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-B73.  
 RX MEDLINE-97303618; PubMed-9159942;  
 RA Gao M., Fisher D.K., Kim K.N., Shannon J.C., Guiltinan M.J.,  
 RT "Independent genetic control of maize starch-branching enzymes IIA and  
 RT IIB. Isolation and characterization of a Sbe2a cDNA."  
 RL Plant Physiol. 114:69-78(1997).  
 CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF  
 CC GLYCOGEN.  
 DR EMBL; U65948; AAB67316.1;  
 DR Mendel; 26099; Zeama; Sbe1; 26099.  
 DR InterPro: IPR000461;  
 DR Pfam; PF00128; alpha-amylase; 1.  
 KW Transferase; Glycosyltransferase.  
 FT NON TER  
 SQ SEQUENCE 814 AA; 91865 MW; 0C88B78127511F38 CRC64;

Query Match 71.8%; Score 3261.5; DB 10; Length 814;  
 Best Local Similarity 74.0%; Pred. No. 3.7e-235;  
 Matches 604; Conservative 70; Mismatches 109; Indels 33; Gaps 5;

OY 36 FNEKFAFSRRVFS-----GKSSHESDSNNMTAKRVLPDGRIEYS 81  
 DB 7 FRRDARSRYVLSCAGAPGVLPVGGSDLLSAPVYDTPQELQTEALIEYKTS 66  
 OY 82 DQLEAPGVSEESQVLTDESILMDKI-----VEDEVNKESVPMRETVSIRKIGS 132  
 DB 67 SPYOTTSVAVAEASGVAEERPELSEYIGVGGTGKIGAGIKAKAPLVE-----E 118  
 OY 133 KPSRIPPGRGORIVDIDPSLGFROHLDYRSQKRLREIDKYEGSLAFSGYKFG 192  
 DB 119 KPRVYIPPGDGQRITYEIDPLBEGFRHLDYRSSEKRRRAIDHDEGLDAFSGYKFG 178  
 OY 193 FSRSEGITYREMAAGATMAALIGDPMNPNADVTONEGWEIFLPPNADGSPPIPH 252  
 DB 179 FTSABEGITYREMAAGASALVGFENMNNADTMRNEGVWEISLPNADGSPAIPH 238  
 OY 253 GSRVAKIRMDTPSGNNDSPANIKFSVOAGELPYNGIYDPEPEEKYVFPKPKRSL 312  
 DB 239 GSRVAKIRMDTPSGVNDSPANIKFPAVOAGELPYNGIYDPEPEEKYVFPKPKRSL 298





CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF  
CC GLUCOGEN.

DR EMBL; Y11282; CAI72154.1; -  
DR Mendei; 16396; Triae; Sbel; 16396.

DR InterPro; IPR000461; -  
DR Pfam; PF00128; alpha-amylase; 1.

KM Signal; Transferase; Glycosyltransferase.

FT SIGNAL 1 54 POTENTIAL.  
FT CHAIN 55 823 1,4-ALPHA-GLUCAN BRANCHING ENZYME II.  
SQ SEQUENCE 823 AA; 92936 MW; 80135FA52CBA4549 CRC64;

## Query Match

Best Local Similarity 71.6%; Score 3254.5; DB 10; Length 823;  
Matches 590; Conservative 84; Mismatches 89; Indels 25; Gaps 6;

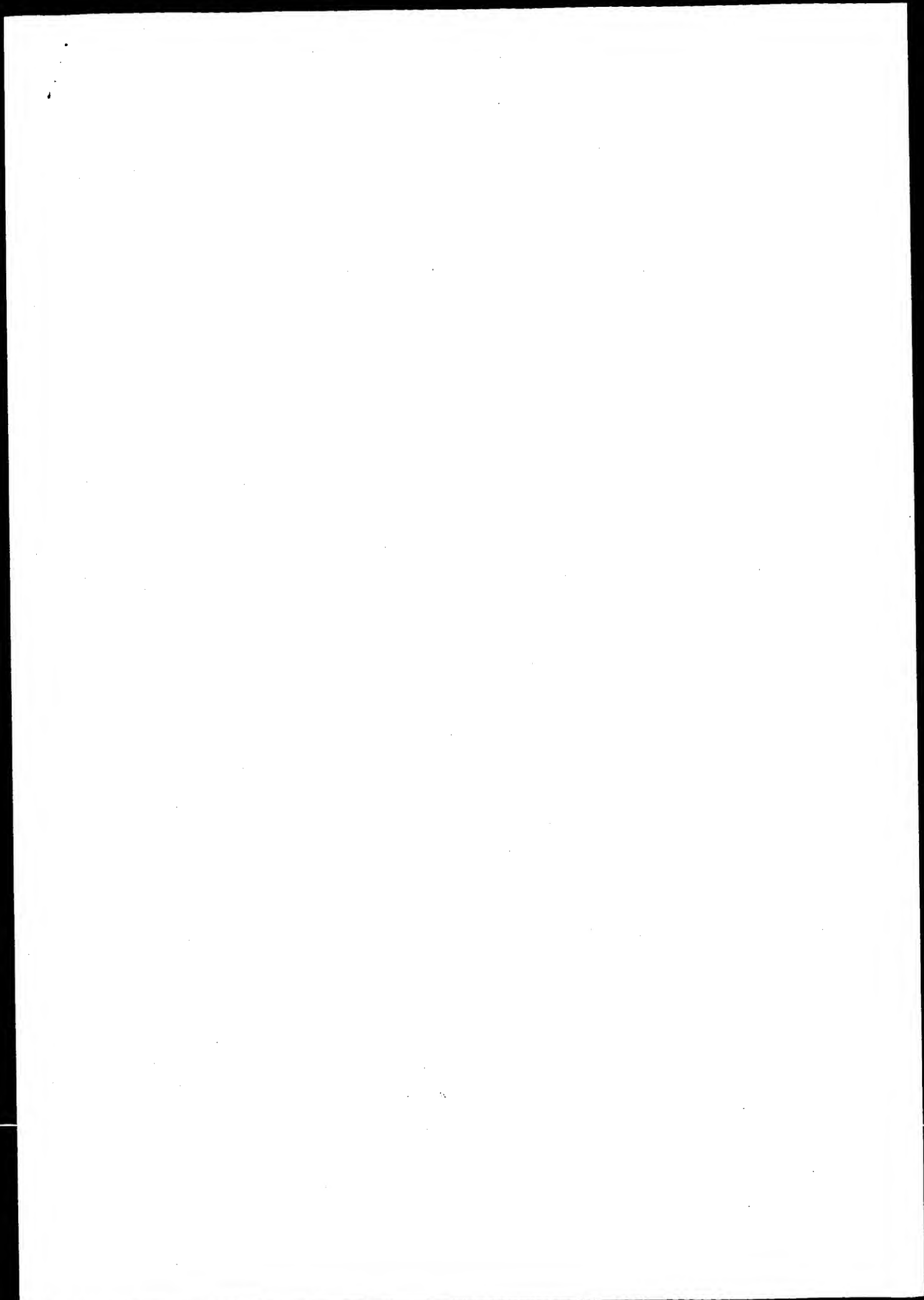
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QY 54 ESDSSNVMWTAS---KRYLPDGRTECYSSSTQDLAPGYSESQYITDYESLMD--- 106
   : || : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 44 KDDSSRAVLSRAASPGKVLVPDG-----ESDDLASPAQ-PEELQIPEDIEEQTAEVNM 95
QY 107 -----DKIVEDEVNK---ESVPMRETVSIRK-IGSKPRISIPPGRCORIVDIDPSLJGF 156
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 96 TGGTAKEKLESSPTQGIYETITDGTAKVKELVYGEKPRVYKPGDGOKITEIDPTLKF 155
QY 157 RQHLDIRYSQYRLAEEDIKTEGSLDAFSKGYEKFGFSRSETGITTYREMAPGATWALIG 216
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 156 RSHLDYRYSERKRIAAIDQHEGGLAEAFSRGKYGFTSAEGITYREMAPGASHALVG 215
QY 217 DENNNPNADVVTONECGVWEIFLPNNADGSPPIPHGSRVKIRMDTPSGKNDISIPAMIKF 276
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 216 DENNNPNADVMTTDDYVWEIFLPNNADGSPALPHGSRVKIRMDTPSGVKSISAMIKF 275
QY 277 SVQADGELPYNGIYDPPPEEKYYFKNPQPKRPSLRIRYESHVGMSTSEPVINTVYANERD 336
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 276 SVQAGEIPIFYNGIYDPPPEEKYYFQHQPKRPSLRIRYESHVGMSTSEPVINTVYANERD 335
QY 337 DYLPRIKELGYNAQVQALAIQESHYASFGYHVTNFYAASSRFGTDDLSLIDKAHELGL 396
   : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 336 EYLPRIKELGYNAQVQALAIQESHYASFGYHVTNFYAPSSRFGTDDLSLIDKAHELGL 395
QY 397 LVLMIDYVSHAFTWLDGLANFDGTDGHYFHSRGRHMMMDSRLLFYNGSWEVLRFLSN 456
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 396 LVLMIDYVSHSSNNLTLDGLNGFDGTDGHYFHSRGRHMMMDSRLLFYNGSWEVLRFLSN 455
QY 457 ARWMLDEKKEFGFEDGVTSMYTHHGLQVDFGTGNYNEYPGATDVAVVYLMILNDMTH 516
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 456 ARWMLDEKKEFGFEDGVTSMYTHHGLQVDFGTGNYNEYPGATDVAVVYLMILNDMTH 515
QY 517 GLPPEAVTIGEDVSGMPTVCIPEEDGVGFDYRLHMAVADKVTETIQKDEDMKMGDIYH 576
   || : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 516 GLHPDAVISIGEDVSGMPTVCIPEEDGVGGLDYRLHMAVADKVTETIQKDEDMKMGDIYH 575
QY 577 MLTNRKWLKCVSYAESHDQALVGDKTIAFWLMDKMDYDPMALDRSTPLIDRGVALHKA 636
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 576 TLTNRKWLKCVSYAESHDQALVGDKTIAFWLMDKMDYDPMALDRSTPLIDRGVALHKA 635
QY 637 IRLITMGLGEGYIINENGNEFGHPEDIDPEPRGLHPGSKFTVPGNNYSYDKCRRRFDLGN 696
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 636 IRLITMGLGEGYIINENGNEFGHPEDIDPEPRGLHPGSKFTVPGNNYSYDKCRRRFDLGN 695
QY 697 SKHLRYHGMQEFDOAIOHLEAYGEMTSEHOYISKDEDRRIIVEEGMLVFNFMHTS 756
   : ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 696 ADPLRKHGMQEFDOAIOHLEAYGEMTSEHOYISKDEDRRIIVEEGMLVFNFMHTS 755
QY 757 SYSDYRVGCLPKPKYKIVLSDDDLFGGFGRLSHDAEHFSFEGWYDNRPSFMVYTPQRT 816
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 756 SFEDYRVGCSRPGKYKVALSDDALRGFSRLDHVDYITTEHPHNNRPSFVTPSRT 815
QY 817 AVYYALVE 824
   ||||| :
Db 816 AVYYALTE 823

```

Search completed: August 7, 2001, 11:20:24  
Job time: 146 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 7, 2001, 11:13:33 ; Search time 25.03 Seconds  
(without alignments)  
2024.836 Million cell updates/sec

Title: US-09-297-703a-29

Perfect score: 4545  
Sequence: 1 MGHYISGIRPCAPLCKSQ.....AVVYALVEDEVENLEFPVAG 836

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A: Geneseq\_0601:\*

- 1: /SIDS8/gcgdata/geneseq/AA1980.DAT:\*
- 2: /SIDS8/gcgdata/geneseq/AA1981.DAT:\*
- 3: /SIDS8/gcgdata/geneseq/AA1982.DAT:\*
- 4: /SIDS8/gcgdata/geneseq/AA1983.DAT:\*
- 5: /SIDS8/gcgdata/geneseq/AA1984.DAT:\*
- 6: /SIDS8/gcgdata/geneseq/AA1985.DAT:\*
- 7: /SIDS8/gcgdata/geneseq/AA1986.DAT:\*
- 8: /SIDS8/gcgdata/geneseq/AA1987.DAT:\*
- 9: /SIDS8/gcgdata/geneseq/AA1988.DAT:\*
- 10: /SIDS8/gcgdata/geneseq/AA1989.DAT:\*
- 11: /SIDS8/gcgdata/geneseq/AA1990.DAT:\*
- 12: /SIDS8/gcgdata/geneseq/AA1991.DAT:\*
- 13: /SIDS8/gcgdata/geneseq/AA1992.DAT:\*
- 14: /SIDS8/gcgdata/geneseq/AA1993.DAT:\*
- 15: /SIDS8/gcgdata/geneseq/AA1994.DAT:\*
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- 18: /SIDS8/gcgdata/geneseq/AA1997.DAT:\*
- 19: /SIDS8/gcgdata/geneseq/AA1998.DAT:\*
- 20: /SIDS8/gcgdata/geneseq/AA1999.DAT:\*
- 21: /SIDS8/gcgdata/geneseq/AA2000.DAT:\*
- 22: /SIDS8/gcgdata/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4545	100.0	836	19	AAW62599
2	3949	86.9	848	19	AAW62600
3	3405.5	74.9	878	18	AAW19113
4	3373	74.2	858	21	AAW39002
5	3356	73.8	882	17	AAW06359
6	3335	73.4	847	17	AAW06400
7	3315	72.9	841	19	AAW41763
8	3309.5	72.8	842	17	AAW3804
9	3241.5	71.3	768	20	AAW06917
10	3219.5	70.8	721	21	AAW39093
11	3180	70.0	825	15	AAW0811

12	3169	69.7	871	19	AAW70895
13	3160	69.5	799	19	AAW6489
14	3159	69.5	799	18	AAW19212
15	3140.5	69.1	693	21	AAW39094
16	2745	60.4	592	21	AAW84410
17	2745	60.4	758	21	AAW84408
18	2710.5	59.6	888	21	AAW84416
19	2377.5	52.3	481	19	AAW62650
20	2192.5	48.2	906	19	AAW71290
21	2192.5	48.2	906	19	AAW69300
22	2130.5	46.9	820	15	AAW53228
23	2124	46.7	751	13	AAW23582
24	2124	46.7	759	13	AAW20896
25	2124	46.7	822	19	AAW56490
26	2124	46.7	844	18	AAW19213
27	2121.5	46.7	820	15	AAW47468
28	2117.5	46.6	833	21	AAW32466
29	2107	46.4	807	20	AAW06916
30	2016	44.4	686	21	AAW49603
31	1597.5	35.1	368	21	AAW15423
32	1592.5	35.0	367	21	AAW15424
33	1426.5	31.4	336	21	AAW15425
34	1242	27.3	228	19	AAW62649
35	940	20.7	212	21	AAW84411
36	927	20.4	212	21	AAW84409
37	576	12.7	762	21	AAW90977
38	572	12.6	639	12	AAW11271
39	571.5	12.6	630	22	AAW69074
40	571.5	12.6	785	19	AAW70886
41	570	12.5	621	21	AAW19285
42	550.5	12.1	731	22	AAW79423
43	542.5	11.9	652	16	AAW80037
44	542.5	11.9	652	17	AAW96109
45	541.5	11.9	753	20	AAW37247

## ALIGNMENTS

RESULT	1	ALIGNMENTS
AAW62599	standard; Protein; 836 AA.	
XX	AAW62599;	
AC	21-SEP-1998 (first entry)	
DT	Cassava starch branching enzyme II (SBE II).	
XX	Starch branching enzyme; SBE; cassava.	
XX	Manihot esculenta.	
XX	WO9820145-A2.	
PN	14-MAY-1998.	
PD	04-NOV-1997; 97WO-GB03032.	
XX	04-NOV-1997; 97WO-GB03032.	
PF	05-NOV-1996; 96GB-0023095.	
PR	(NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.	
PA	Jobling SA, Safford R;	
XX	WPI; 1998-286958/25.	
PI	N-PSDB; AAV38719.	
XX	Starch branching gene from cassava - useful for producing altered	
PT	plants giving modified starch	
XX	Claim 1; Fig 4; 67pp; English.	
PS		
XX		

Maize branching en  
Zea mays starch br  
Corn starch branch  
Arabidopsis thalia  
Amino acid sequenc  
Amino acid sequenc  
Starch branching e  
Potato starch bran  
Rice starch branch  
Branching enzyme.  
Zea mays starch br  
Corn starch branch  
Branching enzyme o  
Maize starch bran  
wSBE I-Dd amino ac  
Glycogen branching  
Arabidopsis thalia  
Arabidopsis thalia  
Starch branching e  
Amino acid sequenc  
N. denitrificans a  
B. stearothermophil  
Aquifex aeolicus V  
Protein encoded by  
A polypeptide with  
Corynebacterium gl  
Bacillus stearothe  
Starch-branching-e  
Protein involved 1



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QY 356 QEHSTYASTGYHTNRYAASSRFGTPDDLSLIDKAHEGLVLMIDIVHSHASTNLDGL 415
D 361 qehsyastgyhtnryaassrfgtpddlslikahelgllvmlidvshasnmldgl 420
QY 416 NMFEDGTGHPFSGRHHMMDSRLFNYSGEVRYFLLSNARKWLDEYKDFGDFPGVT 475
D 421 nmfdgtgthpfsgrrhmmdsrlfnysgevrflfllsnarkwldkydfgdfpgvt 480
QY 476 SMATTHGLQVDFGTGNYMEFGYATDVAVVYLMILNDMIGLPEAVTIGEDVSGMPTV 535
D 481 smatthglqvdfgtgnymeftgyatdvavvylmilmndmiglpeavtigedvsgmptv 540
QY 536 CIPVEDGGVGPYRLHMAVADKWEIIOKRDDEKMGDIYMLTNRRLKCYASASHD 595
D 541 cipvedggvgpyrlhmvadkweilokrddemkgdiymלטnrllkcyasashd 600
QY 596 QALVGDKTIAFWLMDKMDYDPMALDRPSTPLIDRGVALHKMIRLITMGIGEGYLMNMG 655
D 601 qalvgdktafwlmdkmdydpmaldrpstplidrgvalhkmirlitmgigegylnmng 660
QY 656 EFGHEWIDFPRGDLHPSGKFPVGNYSYDKCRREDLGNKRLRYHGMQEFDAIQHL 715
D 661 efghewidfprgdhlpsgkfvpgnysydkcrrredlgnkrlryhgmqefdaiohl 720
QY 716 EEA YGFMTESEHOYISRKDERIRITVEPERGNIVFENFHMWSSSDYRVGCLAKGKRIYL 775
D 721 eea ygmtesehoyisrkderiritevpergnivfenfhmwsssdryvgclakgkriyl 780
QY 776 DSDPLFEGFGRSLSHDAEHSFEGMGYDNRPRSPFVYPTCTAVVYALVED-----EWE 828
D 781 dsdplfegfgrslshdaehsfegmgdydnrprspfvyptctavvyalved-----ewe 840
QY 829 NELEPVAG 836
D 841 nelepvag 848

```

RESULT 3  
AAW19113  
ID AAW19113 standard; Protein; 878 AA.

```

XX AC AAW19113;
XX 26-AUG-1997 (first entry)
XX DE Potato starch branching enzyme II.
XX KW Starch branching enzyme II; beii gene; potato; transgenic plant;
XX KW amylopectin; amylose; starch.
XX OS Solanum tuberosum.
XX FH Key Location/Qualifiers
XX FT Peptide 1.48
XX FT Protein 49..878
XX FT Misc-difference 33
XX FT /note= "residue 33 was not detd. owing to
XX FT Misc-difference 406 degeneracy of coding sequence (codon NTT)"
XX FT /note= "residue 406 was not detd. owing to
XX FT Misc-difference 570 degeneracy of coding sequence (codon TTN)"
XX FT /note= "residue 570 was not detd. owing to
XX FT degeneracy of coding sequence (codon TNT)."
XX PN MO9720040-A1.
XX PD 05-JUN-1997.
XX PF 28-NOV-1996; 96WO-SE01558.

```

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XX 19-APR-1996; 96SE-0001506.
PR 29-NOV-1995; 95SE-0004272.
XX
PA (EKBB/) EK B.
PA (KHOS/) KHOSNOODI J.
PA (LARS/) LARSSON C.
PA (LARS/) LARSSON H.
PA (RASK/) RASK L.
PA (AMTL-) AMTLOGENE HB.
XX
PI Ek B, Khosnoodi J, Larsson C, Larsson H, Rask L;
DR WPI: 1997-310596/28.
DR N-PSDB: AAT69587.
XX
PT Isolated potato starch branching enzyme II - useful for altering
PT degree of amylopectin branching and amylopectin/amylose ratio in
PT potato starch
XX
PS Claim 1; Page 12-15; 24pp; English.
XX
CC The amino acid sequence (AAW19113) for potato starch branching enzyme
CC II (BEII) was deduced from a cDNA clone (AAT69587) isolated from
CC tuber cDNA using primers (AAT69588-89) based on BEII tryptic
CC peptides. It shows 68% identity to potato starch branching enzyme
CC I and about 80% identity to BEII from other plant species. BEII,
CC or functional active parts of the enzyme, can be expressed in
CC transgenic potatoes. The starch obt. from such plants will show a
CC changed pattern of amylopectin branching and an altered amylopectin
CC to amylose ratio.
XX
SQ Sequence 878 AA;

```

Query Match 74.9%; Score 3405.5; DB 18; Length 878;  
Best Local Similarity 72.2%; Pred. No. 0;  
Matches 624; Conservative 91; Mismatches 114; Indels 35; Gaps 5;

```

QY 4 YTGIRFPFCAP-LCKSGSTGFHGYRRTSSCLSFNFKKFAFRVSGKSHSDSSNNVY 62
D 3 ytlsgyrfpfcvpyvksngfssngdrtanxvflkkslsrlaekssyssearptv 62
QY 63 TASKRVL-PDGRICEYSSSTIDQLEAPGVSESOYLTDESLIMD---KIVEEV--- 114
D 63 aasgkvlvpgtqsdsssdgfeftetspenspastdssstmeaagikendavps 122
QY 115 -----NKESVPMREYISIRKIGS-----KPSIIPPGRGQRIYD 148
D 123 sdltgsveeldfssslqldgeygleeskltntseetlidesdrtiregldppglgqklye 182
QY 149 IDPSLTGFROHLDYRSQYKRLREEDIKYEGSLDAPSRGEKFSRSEGTGYREAPG 208
D 183 idpsltgnrghldyrsqkrlreeadikyegsldeafsrgeymgtltsaalclyrewapg 242
QY 209 ATMAALIGDPNKNMNPADYWTONEGWEIPLPNNADSPPIPHGSRVAKIRMDPPSGNKD 268
D 243 agsaallgdfinwdanadimtrnefyveiflfnvdspslprbgsrvklmndpsgykd 302
QY 269 SIPAWIKFSVOAPGELPYNGIYDPPREEKYVFKNPQKRKSLRIYSHVSGMSTEPVI 328
D 303 sipawlnyslqldpdeipnynglydppeeeaylfqhrprkkslriyeshvgmspepki 362
QY 329 NTYANFRDDVLRIRIKLGYNAVALIOEHSGYASFGYHVNPFYFAASRFGTDPDLKSLI 388
D 363 ntyanfrddvldrirklygnavalioehsgyasyfgyhvnlpfayfarsrfgtpddlskll 422
QY 389 DKAHEGLVLMIDIVHSHASTNLDGLMFPDGTGHPFSGRHHMMDSRLFNYSGEVRYFL 448
D 423 dkaheglvlnmidivshasnmldglmldfpgtgyhpfsgrrhmmdsrlfnysgevrflf 482
QY 449 VLRFLLSNARKWLDEYKDFGDFPGVTSMATTHGLQVDFGTGNYMEFGYATDVAVVYAL 508
D 482 vlrfllsnarkwldkydfgdfpgvtsmatthglqvdfgtgnymeftgyatdvavvyal 508

```

Db 483 vlyllsnarwldelfdgdfrtdgvtsmmythhglsvgtfngyeevfglatvdavyl 542  
QY 509 MLNDMTIGLEPEAVTIGEDVSGMPYVCIPEVDEGCGEYFRLHMANVADKWVELIQRDE 568  
Db 543 mlyndllhglpdaifltgedvsgmptlxipvdgvgvdyrlmaladkwelkrtdd 602  
QY 569 WKMDIVMLTNRRLKCVSYAESHDQALVGDKTIAFWIMDKDMYDFMALDRPSPLID 628  
Db 603 wrygdvltltnrrwsekwasyaeshdaqlygdktiafwimdkdmvdfmaldrpsl 662  
QY 629 RGVALLHKIRLTITGLGEGEYINPMGNFHPWIDFPRGDLHLPSCGFVPGNNYSYDKC 688  
Db 663 rglalhknrlrlvtnglsggylnfmgnefghpewidfpnaeghlsdgsyvlpgnqfsgdkc 722  
QY 689 RRRPDLGSKHLRYHGMQEPDQAIQHEAVYGFMTSEHOYISRKDERRIIVERGNLYF 748  
Db 723 rrrldgaeyllyrlyglgeframgyleckyeftlsebqfstrkdegdrmlvfekgnlvf 782  
QY 749 VNFHWTSYSDYRVCGLKPKGKYKIYDSDPDLRGFGRLSHDAEHFSPGCGWYDNRPSPF 808  
Db 783 vnfhwtsysdyrgclpkpkykvalsdplfgyfgridhnaeyftfegwyddrpsl 842  
QY 809 WYTPCRAVAVYALVEDEVENLE 832  
Db 843 mvyapstravayalvdkeeeeee 866  
RESULT 4  
AAC39092 standard; Protein: 858 AA.  
ID AAC39092  
XX AAC39092;  
AC 18-OCT-2000 (first entry)  
DT  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 48321.  
DE  
XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX Arabidopsis thaliana.  
OS  
XX EPI033405-A2.  
FN  
XX 06-SEP-2000.  
PD  
XX 25-FEB-2000; 2000EP-0301439.  
PE  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130691.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 26-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138054.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138647.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139452.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142820.  
PR 09-JUL-1999; 99US-0142977.  
PR 12-JUL-1999; 99US-0143542.  
PR 13-JUL-1999; 99US-0143624.  
PR 14-JUL-1999; 99US-0144005.  
PR 15-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 16-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 19-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144684.  
PR 20-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.



Db 835 aavddddderslvp1 851

# RESULT 5

AAW06399 standard; Protein; 882 AA.

AAW06399;

25-FEB-1997 (first entry)

Class A starch branching enzyme (19con.seq).

Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;

amylose; viscosity; potato.

Solanum tuberosum.

Key Location/Qualifiers

Peptide 1..49

Protein /label= sig\_peptide

Protein /label= mat\_protein

MO9634968-A2.

07-NOV-1996.

03-MAY-1996; 96WO-GB01075.

10-APR-1996; 96GB-0007409.

05-MAY-1995; 95GB-0009229.

(NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.

Cooke D, Debel M, Gidley MJ, Jobling SA, Safford R;

Sidebottom CM, Westcott RJ;

WPI: 1996-506170/50.

N-PSDB; AAT42630.

Class A starch branching enzyme (SBE) has been obtained from

potatoes. In class A SBE moles, a flexible N-terminal domain,

is found, which is not found in class B moles.

Sequence 882 AA;

Query Match 73.88; Score 3356; DB:17; Length 882;

Best Local Similarity 70.98; Pred. No. 7.5e-300; Mismatches 119; Indels 38; Gaps 6;

Matches 617; Conservative 96; Mismatches 119; Indels 38; Gaps 6;

4 YTGIRPCAP-LCKSQSTGFHGYRTTSCLFNFKEAFSRVFSKSSSHSDSSVMV 62

3 YLISGVIFPVSVYKSGFNGSDIRNANVSFLKHSISKLAESYSEIFRSTV 62

63 TARKRVLPDGRICYSSTQLEAPGVSESOVLTVESLIMDD---KIVEDEV--- 114

63 aasgkvlvpgqsdasssstqdfetetspenspactdvestmehasqktendvps 122

115 -----NKSVMKRETVSRKTS-----KPSIPPPGGRORIVD 148

123 sdtgsvveelafasidqdegqgleesktintseetidesdrtrevgipppqgqkiye 182

149 IDPSITGFROHLDRYSQKRLREIDKYESLDLAFSGYKFGFSSEGTITREWAPG 208

183 idpilttyghldyrysgkrlrealdkyeggleafsfryekmgftrsaqilyrewaig 242

QY 209 ATWALIGDFNNMNPADVYTONCEGYVEIFLPNNMDGSPPIPHSGSVKIRMDT PSCNKD 268

Db 243 aqsalligdtrnnwddandimlinefywelflpnnvdgspsaiphgervkrlmdtpgvd 302

QY 269 SIPWIKFSVQAEGLPYNGIYDPPPEEKYVFNQPKRKSIRYESHVGM:STEPY 328

Db 303 sipwlnyslqldpdrlyngydppeeeelylqnpkpkksrlrlyeshlmg:spexk 362

QY 329 NTYANFRDVLPRIKKIGYNAVOLMAIQESHYASFGYHTNTYAAASRGTPEUDLSIT 368

Db 363 nsyvntfdevlprtkklygnalqimalqensyyasfgyhvnltfapsrtrgpcddkssl 422

QY 389 DKAEHLGLVIMDVIHSHASTNTLDGLNMEGDTDGHTFHSGPRGHMMMSRL:NGSGWE 448

Db 423 dkaheglvvlmdlvhshasnntldglnmtdctdscyfhsgargymmwdsrlhngnwe 482

QY 449 VLREPLSNARWMLDEYKFGDFRFDGVTSMYTHGLQVDFGTANYEFGYATDVAVYL 508

Db 483 vlyrlsnarwldafrfdgfrfdgvtssmylthglsvgtfgyeeyfglatdvdavyl 542

QY 509 MLNDMIRGLPEPAVTTIGEDVSGMPVCIPEVDGSGVGFEDRLHMAVADKWEI:OKRDED 568

Db 543 mlvndlthglfpdaltlgedvsgmpfcipvgsgvgfdyrlhmaladkrl:krded 602

QY 569 WKMGDIYHMLNRRWLEKCVSYASHDQALVGDRTIAFWLMDKMDYDFMALDRPSTPLID 628

Db 603 wvrgdlvhlcnrtwsekcvyaaeshdgalvgdktiafwlmdkmdydfmaldrpstplid 662

QY 629 RGVALHKKMIRLITMGLGEGYLFNMGNEFGHPWIDPRDGLH:PSGKFYGNVSYDKC 688

Db 663 rgalhkkmrlitvngl99egylnfmgnefghpewldfrpraeghsdsvlpngjfsydkc 722

QY 689 RRRPDLGSKHRRHNGMDEPOALDHEAAGFMTSEHGYSRKDEDRITVE:RGKMLVE 748

Db 723 rrrldgdaeylryr9ldetdpmylekyemfsehgflstrdegdmvfkgnlvf 782

QY 749 VNFHWTSSYSDYRVGCLKPGKRYKIVLDSDDPLRGFGFRSLSHDHEHSGFEKWNRRPSF 808

Db 783 vnfhwtkysdyrlaclkpgkykvaldsddpll99igrldhnaeyrltegwyddprst 842

QY 809 MYTTPCKRTAVYALV---EDEVENLEPVA 835

Db 843 myapoktaavyalvdkeeeeeevea 872

RESULT 6

AAW06400 standard; Protein; 847 AA.

AAW06400;

25-FEB-1997 (first entry)

Class A starch branching enzyme (psbe2con.seq - clone psj90).

Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;

amylose; viscosity; potato.

Solanum tuberosum.

Key Location/Qualifiers

Peptide 1..11

Protein /label= sig\_peptide

Protein /label= mat\_protein

MO9634968-A2.

07-NOV-1996.

03-MAY-1996; 96WO-GB01075.



Query Match	73.48%	Score 3335	DB 17	Length 847
Best Local Similarity	73.68%	Pred. No. 6e-298		
Matches 608; Conservative	84;	Mismatches 98;	Indels 36;	Gaps 5

[illegible]

FT	/note= "encoded by ambiguous codon"
FT	Misc-difference 811 /label= OTHER
FT	/note= "encoded by ambiguous codon"
FT	Misc-difference 830 /label= OTHER
FT	/note= "encoded by ambiguous codon"
FT	Misc-difference 832 /label= OTHER
FT	/note= "encoded by ambiguous codon"
FT	Misc-difference 838 /label= OTHER
FT	/note= "encoded by ambiguous codon"
FT	Misc-difference 839 /label= OTHER
FT	/note= "encoded by ambiguous codon"
PN	W09634968-A2.
PD	07-NOV-1996.
XX	03-MAY-1996; 96WO-GB01075.
PE	10-APR-1996; 96GB-0007409.
PR	05-MAY-1995; 95GB-0009229.
FX	(NAT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
FA	Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
PI	Sidedottom CM, Westcott RJ;
XX	WPI: 1996-506170/50.
DR	N-PSDB: AAT17267.
XX	New potato plant starch having high amylose content - also class A
PT	starch branching enzyme and corresp. DNA to alter the viscosity of
PT	starch; for use in food, biodegradable products, adhesives, etc.
XX	Example 1; Fig 9; 142pp: English.
XX	Class A starch branching enzyme (SBE) has been obtained from
CC	potatoes. In class A SBE mols., a flexible N-terminal domain,
CC	is found, which is not found in class B mols.
CC	The nucleotide sequence encoding this protein was obtained by
CC	direct sequencing of PCR fragments amplified from first strand
CC	cDNA. Nucleotides which could not be unambiguously assigned are
CC	indicated using standard IUPAC notation. Where this uncertainty
CC	affects the predicted amino acid sequence, x is used in the
CC	sequence.
XX	
XX	Sequence 842 AA:
QQ	
	Query Match 72.8%; Score 3309.5; DB 17; Length 842;
	Best Local Similarity 73.2%; Pred. 1.3e-295;
	Matches 606; Conservative 65; Mismatches 102; Indels 35; Gaps
OY	39 KEAFSRRVFSKSHSDSSNWMTAKRYL-DGRIECSSTDDLEAPGVSESOYL 97
DB	9 khsrlsrklackssyesspstvaasgkvlvpqxsddsssdtdgfetetspenspas 68
OY	98 TDVESLIAMD-----KIVEDEV-----NKESVPAREIVTSIKRIGS----- 132
DB	69 tdvdastmehsqiktenddvepsadtgsveedfdaassqlqgggaLeeskktlnseet 128
OY	133 -----KPSIRPPRGCGRTIYDIDSLTGFRONHLDYRSQYKKRLREEDTKEGSIDAR 184
DB	129 lldesdrirerqipppigskilyeldrlltnyrghllyrysqqkkilrealdkyeggleat 168
OY	165 SRGYKKRFSSSSENGITVRERWAPGTAAALICGFNNNNPNADVTONEGCWVEIFLPNNA 244
DB	168 srgykkmgrftsrtaigtlyrewapqagsaalylgfdnnvdanadimtlrnefygwelflpnv 248

QY 245 DGSPPPHSGRKVTRMDTSGNKDSTIPAMIKFSVOAGELPYNGTYDPPEEKYVFNK 304  
 DB 249 dgsppphsgsrkvtlmdtsgnkdstipamiksvoagelpyngtydppeekyvfkn 308  
 QY 305 QPFRPKSLRTYSHVGMSTSEPIYNTYANFRDVLPRIKKIGYNAVQMAIOESYAS 364  
 DB 309 qpfrpkslrtysghvgsmssepiinsyvnfrdevlprtklgynavqmaiqesyasf 368  
 QY 365 GHVNTFYVAASSRFGTPDDLKSLIDKAHELGLVLMIDIVHSHASTNTDGLNMFDDG 424  
 DB 369 ghvntfyvassrfgtppddlkslidkahelglvmlidvshasntldglnmfddgsc 428  
 QY 425 YHSGRGHMMWMDRLNRYGSEVLRFLSLNARKWLDVEYFDFGRDGVTSMMYTHHGL 484  
 DB 429 yhsgrghmmwmdrlnrygsevlrflslnarkwldveyfdfgrdgvtsmmythhgl 488  
 QY 485 QVDFGNTNVEYGYATDVDAVYLLMLNDMTHGFEPEAVTIGESVGMPTVCIVEGGV 544  
 DB 489 qvdfgntnveygyatdvavylmlndmthgfepeavtigesvgsmpvtciveggv 548  
 QY 545 GEDYLRHAAVADKWEIIOKRDEDMKMGDIYHMLNRRMLEKCVSAESHDAQLVGDKTI 604  
 DB 549 gedylrhaavadkweiiokrdeedmkmgdiyhmlnrrmlekcvsaseshdaqlvgdkti 608  
 QY 605 AFWLMDKMDYPMALDRPSTPLIDRGVALHMKIRLITMGIGESYTLNFMKNEFGHPED 664  
 DB 609 afwlmdkmdypmaldrpstplidrgvalhmkirlitmgigesytlmfknefghpewid 668  
 QY 665 FPRGDLHPSKFEVPGNNYSYDKCRFRDLGNSKHLRYHGMQEDQAOIHLFEAYGPM 724  
 DB 669 fprgdlhpskfevpgnnysydkcrfrdlgnskhlryhgmqeedqaoihlfeaygpm 728  
 QY 725 EHOYSRKDEDRILIVERGNLVFVFNHTSSSIDRVGCLKPGKXKIVLSDSDPLFG 784  
 DB 729 ehoyrkeddrilivergnlvfvfnhtsssidrvvgclkgkxkivlsdspdplfg 788  
 QY 785 FGRSLHDAEHPSFEGWYDNRPSPVYTPCRAFTAVYALVDEVEENLE 832  
 DB 789 fgrslhdaehpsfegwydnrpspvtytpcraftavyalvdeveennele 835

## RESULT 9

AAY06917  
 ID AAY06917 standard; Protein; 768 AA.  
 AC AAY06917;

05-JUL-1999 (first entry)  
 DE Starch branching enzyme II (SBE II) amino acid sequence.  
 XX

KW Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBSS;  
 KW starch branching enzyme; starch soluble synthase; debranching enzyme;  
 KW endosperm; wheat; barley; granule-bound synthase; glutenin; starch;  
 KW grain softness protein I; bacterial isomylase; glycogen synthase;  
 KW WSB I-D4 gene.  
 XX

XX Trifolium tauschii.  
 OS

XX MO914314-A1.  
 PN

XX 25-MAR-1999.  
 PD

XX 11-SEP-1998; 98WO-AU00743.  
 PF

XX 20-MAR-1998; 98AU-0002509.  
 PR

XX 12-SEP-1997; 97AU-0009108.  
 XX

PA (CSTR) COMMONWEALTH SCI & IND RES ORG.  
 PA (GOOD-) GOODMAN FIELDER LTD.  
 PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.  
 PA (AUSU) UNIV AUSTRALIAN NAT.  
 XX

PI Li Z., Morell M., Rahman S;  
 XX  
 DR WPI; 1999-229525/19.  
 XX  
 PT New isolated cereal plant enzyme genes used for, e.g. expression of  
 PT antisense sequences of granule bound synthase  
 XX  
 PS Disclosure: Page 83-85; 171pp; English.

CC The invention relates to a novel enzyme of starch biosynthetic pathway  
 CC in a cereal plant, where the enzyme is selected from starch branching  
 CC enzyme (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching  
 CC enzyme (DBE), with the proviso that the enzyme is not SSS I of rice, or  
 CC SBE I of rice or maize. The methods and products can be used for  
 CC targeting expression specifically to the endosperm of the seeds of cereal  
 CC plants such as wheat or barley. They can be used for the expression of  
 CC e.g. antisense sequences of granule-bound synthase (GBSS), SBE II, low  
 CC mol. wt. glutenin, grain softness protein I, bacterial isomylase,  
 CC bacterial glycogen synthase, and wheat high mol. wt. glutenin Bx17. They  
 CC can be used for modifying the characteristics of starch produced by a  
 CC plant. The present sequence represents the SBE II protein sequence.

SQ Sequence 768 AA;

Query Match 71.3%; Score 3241.5; DB 20; Length 768;

Best Local Similarity 77.2%; Pred. No. 2,1e-289;

Matches 582; Conservative 78; Mismatches 83; Indels 11; Gaps 2;

QY 78 SSSTDLBPATVSEESQVLT-----DVESLTMDKIVEDVKNESVPMRETVSRKI 130  
 DB 19 aaqeeelqpedieaeaynmimgtaeklessepgqivelttdtygvvelv----- 74  
 QY 131 GSKPRSTPPRGGRITDIDPSLTGFRQHLDIRYQYKRLREIDKYESGLDAFSNGYK 190  
 DB 75 gekprvvpkpgdgklyelidpkltdirshldryseyrriraaidqheglaefarygk 134  
 QY 191 FGFSRSEGTITRRMAGATMAALIGDFNNMNPADVMTONEGWEIIFLNNAGSPRI 250  
 DB 135 lgftrsaeglttrmwpaghsaalvgdfnmnpadmtlctdgyvelltlnpnadgspl 194  
 QY 251 PHGSRVTRMDTBSGNKDSIPAMIKFSVOAGELPYNGTYDPPEEKYVFNKPKRP 310  
 DB 195 phgsrvtrmdtbsgvkdsipamiksvoagelpyngtydppeekyvfknpkxrpe 254  
 QY 311 SLRTYSHVGMSTSEPIYNTYANFRDVLPRIKKIGYNAVQMAIOESYASFGYHTN 370  
 DB 255 slrtysghvgsmssepiinsyvnfrdevlprtklgynavqmaiqesyasfgyhtn 314  
 QY 371 FYAASSRFGTPDDLKSLIDKAHELGLVLMIDIVHSHASTNTDGLNMFDDG 430  
 DB 315 fyaassrfgtppddlkslidkahelglvmlidvshasntldglnmfddgsc 374  
 QY 431 RGHMMWMDRLNRYGSEVLRFLSLNARKWLDVEYFDFGRDGVTSMMYTHHGLQVDTG 490  
 DB 375 rghmmwmdrlnrygsevlrflslnarkwldveyfdfgrdgvtsmmythhglqvdtdg 434  
 QY 491 NYNEFYGATDVDAVYLLMLNDMTHGFEPEAVTIGESVGMPTVCIVEGGV 550  
 DB 435 nynefygatdvavylmlndmthgfepeavtigesvgsmpvtciveggv 494  
 QY 551 HMAVADKWEIIOKRDEDMKMGDIYHMLNRRMLEKCVSAESHDAQLVGDKTI 610  
 DB 495 hmaavadkweiiokrdeedmkmgdiyhmlnrrmlekcvsaseshdaqlvgdkti 554  
 QY 611 KMDYDFMALDRPSTPLIDRGVALHMKIRLITMGIGESYTLNFMKNEFGHPED 670  
 DB 555 kmdydfmaldrpstplidrgvalhmkirlitmgigesytlmfknefghpewid 614  
 QY 671 HLPSCGFVPGNNYSYDKCRFRDLGNSKHLRYHGMQEDQAOIHLFEAYGPMSEHOYIS 730  
 DB 615 hlpsgfvpngnnysydkcrfrdlgnskhlryhgmqeedqaoihlfeaygpmsehoys 674



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PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148365.
PR 16-AUG-1999; 99US-0148384.
PR 17-AUG-1999; 99US-0149368.
PR 18-AUG-1999; 99US-0149175.
PR 20-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 23-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150366.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 06-OCT-1999; 99US-0157753.
PR 07-OCT-1999; 99US-0157865.
PR 08-OCT-1999; 99US-0158029.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 14-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159337.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 22-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 26-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match 70.8%; Score 3219.5; DB 21; Length 721;  
 Best Local Similarity 81.5%; Pred. No 2e-287;  
 Matches 573; Conservative 66; Mismatches 61; Indels 3; Gaps 1;

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QY 135 RSTPPGKQRIYDIPSTIGFQHLADYRYSQYKRLREIDKYSGLDASRGYKFGFS 194
DB 12 Rklppgdgkriydidpmishmldyrygyrkliireidkneqgleafsfgyelfgt 71

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QY 195 RSEFGITTYEMAPGATMAALIGDFNNMNPADVMTQNEGYEITFLPNMADGSPPIPHGS 254
DB 72 ratstgityrewaggaakaasllidgfnnnakadmarndfgywelflpnnadgsaiphgs 131
QY 255 RYKIRMDPSSGNKDSIPAKIRFSVQABCELYNGIYDPEEERYKVRKNDPKPKSLRT 314
DB 132 rtklrmtdcpsgikdsipawikysvpgpelnyngvvydppcedkyatkhprrpkkslrl 191
QY 315 YESHVGMSSTEEPIVNTYANFNRDVLPRIKILGYANAOVLMIOESYASGCVHTNFYAA 374
DB 192 yeshvgmsstepekintyanfrddvlprikilgyanaqmaqenayasygynvthflap 251
QY 375 SREFGTPDDLKSLDKAHELGLVLMIDIVHSHASTNTLDGLNMFEDGDGHYFSGRGNH 434
DB 252 ssrfgtpddlksldkahlglvlmidivhshakntldglndgdggyflnsgsrgyh 311
QY 435 WMMDSRLFNYSWEYLRLPLSLNARWMLDEYKFGDFRRDGYTSMAVYTHHGLQVDFGNVNE 494
DB 312 wmmdsrlfnysweylrplslsnarwmldeykgfdgfrdgytsmvythhglqveflgnyne 371
QY 495 YFGYATDVDAVYVYLMNDMTIHGLFPEAVTIGEDVSGMPVCIPEDDGGYGFYRLHNAV 554
DB 372 yfgystdvdaavyvlymlndmthglfpeaivvgedvsgmpafcvpeedggygfyrlhnav 431
QY 555 ADKWEITQKDEDMKMGDIYHMLTNRRLKCYSAESHDAQLVGDKTIAFWLMDKDMY 614
DB 432 adkwelitqkdedmkmgdiyhmltnrrmlkcyasaeshdaqlvgdkctafwlmkdmxy 491
QY 615 DFMALDRSTPLIDRGVALHMKMPLITMGISGEGYINFMKNEGHENIDFPRGDLHLPS 674
DB 492 dfmavdrstplidrgvalhmkmlplitmglsgegylnfmneghenidfpregdlhlps 551
QY 675 GKFPVGNNSYDCKRRPFDLGNSKHLRYHGMQEPDQAIQHLAEYFMTSEHOYTSRKE 734
DB 552 gkfvpgnnysydkrrpfdlgnskhlryhgmqepdqaqlhlaeyfmtsehoystsrke 611
QY 735 RDRITVEFEGNLTVEFNFHTSSYSDYRVGCLRPKRYKIVLSDDBLFGGFRSLSHDAEH 794
DB 612 gdrivtergnltvfnhtssysdyrvgclrpkykivlssdbblfggfrslshdah 711
QY 795 FSPFEGWYDNRRPSFMVYTPCPTAVVYALVEDEYENE---LEPV 834
DB 672 ftsdgrndrpscfmyaportavyaavddddderslvp 714

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RESULT 11  
 ID AAR60811 standard; Protein; 825 AA.  
 AC AAR60811;

DT 05-JUL-1995 (first entry)

DE Rice starch branching enzyme.

KW Starch branching enzyme; rice; starch content.

OS Oryza sativa.

FN Key Location/Qualifiers

FT Peptide 1..65

FT Protein /label- transit-Deptide

PN JP06261767-A.

PD 20-SEP-1994.

PF 22-OCT-1993; 93JP-0265171.

PR 29-OCT-1992; 92JP-0291719.

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XX (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
XX WPI: 1994-37418/42.
XX DR N-PSDB: AAO73750.
XX PT New gene of branching enzyme of rice starch - useful for
XX PT increasing starch yield of rice grains
XX PS Claim 1: Page 9-12; 13pp; Japanese.
XX CC The rice starch branching enzyme (AAR60811) and cDNA encoding it
XX CC have been isolated. The starch content of rice grains can be
XX CC increased by increasing the expression of branching enzyme in
XX CC rice plants.
XX SQ Sequence 825 AA:

Query Match 70.0%, Score 3180; DB 15; Length 825;
Best Local Similarity 70.3%, Pred. No. 1.1e-283;
Matches 586; Conservative 87; Mismatches 116; Indels 44; Gaps 7;

9 IREPCAPLCKSOSTGFHGYRTSCLSFNFKAERSRVFSKSSHSDSSVMYATAS--- 65
20 vrfpv-----pagarvraaaelp-----srlslsgrirfgavrvvgsqgrvavraagas 70
66 -KRLPDGRLE--CVSSSTDQLEAPGVSE-----ESQVLNDESLLMDKIVE 111
71 gevmlpegesdgmprvagsddqlpaldelstevegaelessgsdvegv---krvv 126
112 DEVNKSVPKRETVSIRKIGSKPRSIIPPGRGORITVDPSLTGRFRLHDIRYSQYKRLR 171
127 eelaae-----qkprvvpplgddqkifgmssmngkykhlleyralsyrrlr 172
172 EELDKYEGSLDARSRGYERKFSRSETGITYREMAFGATMALIDFPNNMNPNDVMTON 231
173 sdldqyegjletstisrgefghaegytyrewaggaahsaalvgdfnmwpmadmkn 232
232 ECGWETELFNNMADSPRPHGSRVKIRMDTPSGNKDSIPAMIKFSVOAPGLPYNGIY 291
233 etgweilfpmnadsaprlphgsrvrvmetpsgikdsipavikysvgaagipnglyy 292
292 DPEPEEKYVRKNQPKRKSLRTYESHVGMSSTEPYINTYANPRDVPRIKILGYNAVO 351
293 dpeeeekylikhpqkpkrlrlyelcivngmsstepkincyanfridevprliklgynavq 352
352 LMAIQEHSYVASTGYHVTNFTYAASSRGPDPDLKSLIDKAHELGILYMDIYHSHASTNT 411
353 lmaiqehayysfgyhvtntfapsstfgrpedklsldkanehlgilvmdvshasnt 412
412 LDGILNMFDTGDGAFHSGPRGHMMWDSRLFNYSWEVYLFELISNARWMLDEYKDFPF 471
413 ldglnfdgldthfghsgrghmmwdsrlfnyswevylfllsnaerwmldeekfgrf 472
472 DGVTSMATYTHHGLOVDFTGNYNEFGYATDVAVVYLMILNDMIHCLPFAVTIGEDVSG 531
473 dgvtssmatyhhglovdftgnynefgyatdvavvylmilmndmihclpfavtigedvsg 532
532 MPTVCIPEDGGVGFEDRLHMAVADKWEILIOKRDDEDMKGDIVHMLITNRMLERKCVSYA 591
533 mptvcipedggvgfgydylrllmaavpdkwlellkgsdeswmgdvlhcltnrrvsekcvya 592
592 ESHQALVGDCTIAFWLMDKMYFEMALDRSPPLIDRGVALHMKMLRLITMGISGEGYIN 651
593 eshqalvgdctiafwlmdkmyfemaldrspplidrgvalhmkmlrlitmgisggyin 652
652 FMGNFEGPEWIDPRGDLHPSGKFPVGNVSYDKCRFRPFDGNSHLEHYHMOEFDOA 711
653 fmgnfegpewidprapqvlpsngkflpnmnsydkcrrffidgdaadylyrygmlefda 712
712 IOHLEAAGFMUTSEHOYISRKDERDRIIVERKMLVYVFNFWHTSSSDVRVCLPKGX 771

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Db 713 mqsleekygmtsdhngyisrkheedkmlilekgdlvfvfnfmsnsyfyivgckpkpy 772
Qy 772 KIVDSDDPLEGGFGGRSLSHDAEHFSEGWYDNRRSPMYTTPCKRAVYALVE 824
Db 773 kvvdsdaglfgfgrlhtaehtcdshndrpfysfsyvspilcvyapae 825

RESULT 12
AAW70895
ID AAW70895 standard; protein; 871 AA.
AC AAW70895;
DT 23-AUG-1999 (first entry)
DE Maize branching enzyme II.
KW Non-glycogen-like polysaccharide production; fermentation;
KW starch synthesis enzyme; glycogen-synthesis enzyme; glycogen synthesis;
KW non-starch branching gene; amylopectin; amylose; plant-like starch;
KW maize branching enzyme II.
OS Zea mays.
PN MO9844780-A1.
PD 15-OCT-1998.
PF 03-APR-1998; 98WO-US06660.
PR 04-APR-1997; 97US-0042939.
PA (EXSE-) EXSEED GENETICS LLC.
PT Guan H, Keeling PL;
PT N-PSDB: AAW70861.
DR WPI: 1998-568285/48.
XX N-PSDB: AAW70861.
XX Producing non-glycogen-like polysaccharides in bacteria, fungi or
XX plants - transformed with genes for enzymes involved in starch or
XX glycogen synthesis allows fermentative production of starches with
XX engineered properties
XX Disclosure: Fig 53; 150pp; English.
XX The specification describes a method for the production of
XX non-glycogen-like polysaccharides in a host. The method comprises
XX transforming a host, suitable for fermentation, with genes encoding
XX starch- or glycogen-synthesis enzymes, and fermenting the transformants.
XX The specification also describes hosts transformed with a gene active
XX in glycogen synthesis and at least one non-starch branching gene,
XX involved in production of amylopectin or amylose in its original host.
XX The method is used to produce plant-like starches by fermentation and
XX new starches in plants. These starches are useful for all food and
XX non-food applications of starch. The present sequence is used in
XX the course of the invention.
XX SQ Sequence 871 AA:

Query Match 69.7%; Score 3169; DB 19; Length 871;
Best Local Similarity 70.4%; Pred. No. 1.2e-282;
Matches 584; Conservative 84; Mismatches 93; Indels 68; Gaps 8;

2 GHYTSIGRPPCAPLCKSOSTGFHGYRTSCLSFNFKAERSRVFSKSSHSDSSVMY 61
33 glftrgavgc-----sgltgmrar-----aaarka-----ym 62
Qy 62 VTAKRYLPDG--RIECYSSSTDQLEAPGVSEESQV---LTDVSLMDKXIYEDVN 115
Db 63 vpegen---dqlaarsadsaqfqsdelevp-diseeltcgayvadagat----- 106

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QY 116 KESVPMRETVSIRKIGSKPRSIPPRGQRITYDIDPSLTGFRQHLDYNSQKRLREED 175
Db 107 -----nrvvpppsdqkllfqldpmlqgkykylleyrsllyrrltdid 150
QY 176 KYEGSLDAFSRGEKFGESRSETGITYREMAPGATWALIDGFNNMNPNAVMQNECGV 235
Db 151 ehggldafsrsgyefgnfnraaegilyrewapgaaisaalygdlnwppndrmknefyv 210
QY 236 WEILFNNADSPRIPIHSGSRKIRMDTPSGNKSIPANIKFSVOAPGFLPNNGIYYDPE 295
Db 211 weiflpmnadgtsplphgsrkvkrmdtpsglkdslpawlkysvqapgeipydgiyydppe 270
QY 296 EEKYVFKNPQKRRKSLRIYESHVGMSTEPYINTYANFRDVLPRIKKLGNVQMLAI 355
Db 271 evkyvfrhaqpkrrkslriyethygmsspepkintynfridevlprikklgynaavqlmai 330
QY 356 QEHSYVASFGEYHVTNFEYAASSRFGTDDLSLIDKAHELGILVLMQDVHSHASNTDGL 415
Db 331 qehsyysfgyhvtntfapsrftgpeelnsldraheglvlmdvshassnltldgl 390
QY 416 NMEDGTGHRFHSGRGHMMMDSLRPNYSWEVLRLLSNARWMLDEYKFRDFDGYT 475
Db 391 ngfdgtchhyfhsgrghmmwdsrlfngynewelrflfnsarwleeykfdgfrfdgyt 450
QY 476 SMATYTHGLQVDFGTGNNEFYGYATDVAVYYLMLNDMTHGLFPEAVTIGEDVSGMPTV 535
Db 451 smmytthnglqvtfgntheeyfgfatdvavyylmvndlthgilypeavtligedvsmpftf 510
QY 536 CIPVEDGSGVDYRLHMAVADKWELIQRDEBWKMGDIYHMLTNRRWLKCVSYAESHD 595
Db 511 alpyhdsgvgfdyrmhnavadkwidlkgdsdetkwmgdlvhltnrrwlkcvlyaeshd 570
QY 596 QALVGDKTIAFWLMDKMYPMALDRPSTPLDRGVALHMKIRLITMGLGEGEYLNMGV 655
Db 571 qalvgdktiafwlmdkmydimaldrpstpldrvalhmkirlltmglgsegylntfmgv 630
QY 656 EFGFHEIDPPRGDLHPSGKFPVGNMYSYDKRRRDLGNSKHLRKHQOEFOALQHL 715
Db 631 efgfhpeidfprrgdlpsgkflpgnmysydkcrrtldgdayllyhgmqefdgamql 690
QY 716 EBAVGEWTSEHOYISRKEDRRIIVEERNLVFVFNHMTSSYSDYRVCGLKPGKYIYL 775
Db 691 eqkyefmtsdhyisrkhedkvlvfeqglvfvfnhcnmsyfdyrrlgcrkpgykvvyl 750
QY 776 DSDDPLEFGGGRSLSHAENHSEFGWTDNPRSRMVTTPCCTAAVYALVE 824
Db 751 dsdaglfgfgrslshaehntadcsdnrpyfsyvtprtcvvyapve 799

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## RESULT 13

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AAW56489
ID AAW56489 standard; Protein; 799 AA.
AC AAW56489;
XX
XX
XX 11-SEP-1998 (first entry)
XX
XX
XX Zea mays starch branching enzyme II.
XX
XX SER; starch-encapsulating region; fusion vector;
XX starch branching enzyme II; glucosyl transferase.
XX
XX Zea mays.
XX
XX WO9814601-A1.
XX
XX 09-APR-1998.
XX
XX 30-SEP-1997; 97WO-US17555.
XX
XX 30-SEP-1996; 96US-0026855.
XX
XX (EXSE-) EXSEED GENETICS LLC.
PA

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XX
XX Guan H, Keeling P.
PI
PI WPI, 1998-240100/21.
DR
DR N-PSDB; AAV29757.
XX
XX
XX Hybrid polypeptide comprising starch-encapsulating region and
PT protein - useful for, e.g. producing protein(s) resistant to
PT degradation by stomach acids
XX
XX Example 2; Page 43; 156pp; English.
XX
XX The sequence is that of starch branching enzyme II.
CC It can be used in the production of a hybrid polypeptide
CC comprising a starch-encapsulating region (SER) fused
CC to a payload protein. The hybrid polypeptide can be used to make
CC modified starches comprising the payload protein, selected from,
CC e.g. hormones, growth factors, antibodies, enzymes, dyes,
CC immunoglobulins, etc. The modified starch can also be used
CC to provide grain feeds enriched in amino acids. By encapsulating
CC the payload protein in starch, it is more resistant to
CC degradation by stomach acids.
XX
XX Sequence 799 AA:
SQ

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## Query Match

Best local similarity 70.3%; Score 3160; DB 19; Length 799;

Matches 583; Conservative 83; Mismatches 95; Indels 68; Gaps 8;

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QY 2 GHATYISGIRFPCCAPILCKSSQSTGFHGRYRRTSCLSFNFKEAFRRYFSGKSHESDSSNMV 61
Db 33 glfltrgavgc-----sglthgamraa-----aaarka-----vm 62
QY 62 YIASKRVLPDG---KECYSSSTDOLEAPGVSESOV---LTVESLIMDKIVEENV 115
Db 63 vpegen---dgiasrdsaqfsgdelev-diseetcgayadaqal----- 106
QY 116 KESVPMRETVSIRKIGSKPRSIPPRGQRITYDIDPSLTGFRQHLDYNSQKRLREED 175
Db 107 -----nrvvpppsdqkllfqldpmlqgkykylleyrsllyrrltdid 150
QY 176 KYEGSLDAFSRGEKFGESRSETGITYREMAPGATWALIDGFNNMNPNAVMQNECGV 235
Db 151 ehggldafsrsgyefgnfnraaegilyrewapgaaisaalygdlnwppndrmknefyv 210
QY 236 WEILFNNADSPRIPIHSGSRKIRMDTPSGNKSIPANIKFSVOAPGFLPNNGIYYDPE 295
Db 211 weiflpmnadgtsplphgsrkvkrmdtpsglkdslpawlkysvqapgeipydgiyydppe 270
QY 296 EEKYVFKNPQKRRKSLRIYESHVGMSTEPYINTYANFRDVLPRIKKLGNVQMLAI 355
Db 271 evkyvfrhaqpkrrkslriyethygmsspepkintynfridevlprikklgynaavqlmai 330
QY 356 QEHSYVASFGEYHVTNFEYAASSRFGTDDLSLIDKAHELGILVLMQDVHSHASNTDGL 415
Db 331 qehsyysfgyhvtntfapsrftgpeelnsldraheglvlmdvshassnltldgl 390
QY 416 NMEDGTGHRFHSGRGHMMMDSLRPNYSWEVLRLLSNARWMLDEYKFRDFDGYT 475
Db 391 ngfdgtchhyfhsgrghmmwdsrlfngynewelrflfnsarwleeykfdgfrfdgyt 450
QY 476 SMATYTHGLQVDFGTGNNEFYGYATDVAVYYLMLNDMTHGLFPEAVTIGEDVSGMPTV 535
Db 451 smmytthnglqvtfgntheeyfgfatdvavyylmvndlthgilypeavtligedvsmpftf 510
QY 536 CIPVEDGSGVDYRLHMAVADKWELIQRDEBWKMGDIYHMLTNRRWLKCVSYAESHD 595
Db 511 alpyhdsgvgfdyrmhnavadkwidlkgdsdetkwmgdlvhltnrrwlkcvlyaeshd 570
QY 596 QALVGDKTIAFWLMDKMYPMALDRPSTPLDRGVALHMKIRLITMGLGEGEYLNMGV 655
Db 571 qalvgdktiafwlmdkmydimaldrpstpldrvalhmkirlltmglgsegylntfmgv 630

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PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127465.  
PR 06-APR-1999; 99US-0128233.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 21-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
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DB 302 llsnarwmldeykdfrrfgsvtsmatthglovdftgnynefgyatsdvavvyvlymnl 361  
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5	1635.5	36.0	566	4	US-08-104-158-2
6	542.5	11.9	652	4	US-08-528-026C-4
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RESULT 1
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; Sequence 2, Application US/09087277B
; Patent No. 6169226
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/087, 277B
; CURRENT FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: PCT/SE96/01558
; EARLIER FILING DATE: 1996-11-28
; EARLIER APPLICATION NUMBER: SE 9504272-7
; EARLIER FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: SE 9601506-0
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 878
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: bell gene (branching enzyme II
US-09-087-277-2

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RESULT 2
US-08-941-445A-15
: Sequence 15, Application US/08941445A
: Patent No. 6107060
:
: GENERAL INFORMATION:
: APPLICANT: Keeling, Peter
: APPLICANT: Guan, Haining
: TITLE OF INVENTION: Starch Encapsulation
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
: STREET: 5370 Manhattan Circle
: CITY: Boulder
: STATE: CO
: COUNTRY: US
: ZIP: 80303
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/941,445A
: FILING DATE: 30-SEP-1997
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/026,855
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FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-941-445A-15

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Best Local Similarity 70.3%; Pred. No. 2,4e-299; Indels 68; Gaps 8;
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571 QALVGDKTIAFWLMDKMDYFMDLRSTPLIDRGVALHKTMLITMGLGGGYLNFEMNG 630
656 EFGHEWIDFPRGDLHLPSCGFYVGNYSYDKCRREFDIGNSKHLRYGMOFDOALIOHL 715
631 EFGHEWIDFPRGDLHLPSCGFYVGNYSYDKCRREFDIGNSKHLRYGMOFDOALIOHL 690
716 EAVAGFMTSEHOYSRKDEPRRIYFERGNLVEVFNFWHTSSYSDYRGVCKLPKRTKIYV 775
691 EQKYEFTMSDHOYISRKDEPRRIYFERGNLVEVFNFWHTSSYSDYRGVCKLPKRTKIYV 750
```

QY 776 DSDPFGGRLSHDAHEFSEFGWYDNRPSRMYTPCRTAVYALVE 824  
 DB 751 DSDAGLFGGFSRIHHAHEFTADCSHNRPSFSVTYPSRTCYAYAVE 799

## RESULT 3

US/09/087  
 ; Sequence 4, Application US/09087277B  
 ; Patent No. 6169226  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EK, Bo  
 ; APPLICANT: KHOSNODI, Jamshtid  
 ; APPLICANT: LARSSON, Clas-Tomas  
 ; APPLICANT: LARSSON, Hakan  
 ; APPLICANT: RASK, Lars  
 ; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO  
 ; FILE REFERENCE: 003300-486  
 ; CURRENT APPLICATION NUMBER: US/09/087, 277B  
 ; EARLIER APPLICATION NUMBER: 1998-05-29  
 ; EARLIER FILING DATE: 1996-11-28  
 ; EARLIER APPLICATION NUMBER: SE 9504272-7  
 ; EARLIER FILING DATE: 1995-11-29  
 ; EARLIER APPLICATION NUMBER: SE 9601506-0  
 ; EARLIER FILING DATE: 1996-04-19  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 464  
 ; TYPE: PRT  
 ; ORGANISM: Unknown  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Unknown Organism: be11 gene fragment (branching enz  
 US/09/087, 277-4

Query Match 48.5%; Score 2204; DB 4; Length 464;  
 Best Local Similarity 84.0%; Pred. No. 2e-206;  
 Matches 389; Conservative 40; Mismatches 34; Indels 0; Gaps 0;

QY 240 LPNNADGSPPIPHGSRVKIMDTPSGNKSIPAMIKFSVQAPGLPYNGIYDPPPEEKY 299  
 DB 1 LPNNVDSGSPPIPHGSRVKIMDTPSGNKSIPAMIKFSVQAPGLPYNGIYDPPPEEKY 60  
 QY 300 VFNPPQPKRKSRIYESHVGMSTBPVINTYANFRDVLPRIKLGYNAVOLMAIOEHS 359  
 DB 61 IFQHPKPKRKSRIYESHVGMSTBPVINTYANFRDVLPRIKLGYNAVOLMAIOEHS 120  
 QY 360 YVASFGYHTNFAAASRGTDPDDLSLDKAHEGLVLMDIVHSHASTNTLDGIMFD 419  
 DB 121 YVASFGYHTNFAAASRGTDPDDLSLDKAHEGLVLMDIVHSHASTNTLDGIMFD 180  
 QY 420 GIDGHYFHSGPRGHMMWMSRLFNYSWELRFLSNARWMLDEYKDFRFDGVTSMY 479  
 DB 181 GIDSCYFHSGPRGHMMWMSRLFNYSWELRFLSNARWMLDEYKDFRFDGVTSMY 240  
 QY 480 THHGLOVDTGNTNEXFYATDVDAVYIMLNDMHLGFPRAVITIGEYSGMPYVCIYV 539  
 DB 241 THHGLOVDTGNTNEXFYATDVDAVYIMLNDMHLGFPRAVITIGEYSGMPYVCIYV 300  
 QY 540 EDGCVGFYDLRLHMAVADKWEIIOQRDEDMKMDIYHMLTNRWLEKCVSYASHDQALY 599  
 DB 301 EDGCVGFYDLRLHMAVADKWEIIOQRDEDMKMDIYHMLTNRWLEKCVSYASHDQALY 360  
 QY 600 GDKTIAFWLMDKMDYDMLADRPSTPLIDRGVALHMKMRLTMGLGEGYLNFMGNEGH 659  
 DB 361 GDKTIAFWLMDKMDYDMLADRPSTPLIDRGVALHMKMRLTMGLGEGYLNFMGNEGH 420  
 QY 660 PEKIDPPRGDLHPSGKFPVGNYSYDKCRRRPDLGNSHLRY 702  
 DB 421 PEKIDPPRGDLHPSGKFPVGNYSYDKCRRRPDLGNSHLRY 463

## RESULT 4

US-08-941-445A-17  
 ; Sequence 17, Application US/08941445A  
 ; Patent No. 6107060

; GENERAL INFORMATION:  
 ; APPLICANT: Keeling, Peter  
 ; APPLICANT: Guan, Hanning  
 ; TITLE OF INVENTION: Starch Encapsulation  
 ; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
 ; STREET: 5370 Manhattan Circle  
 ; CITY: Boulder  
 ; STATE: CO

; COUNTRY: US  
 ; ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/941,445A  
 FILING DATE: 30-SEP-1997  
 CLASSIFICATION: 800

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/026,855  
 FILING DATE: 30-SEP-1996

ATTORNEY/AGENT INFORMATION:  
 NAME: Winner, Ellen P  
 REGISTRATION NUMBER: 28,547

REFERENCE/DOCKET NUMBER: 89-97  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 499-8080  
 TELEFAX: (303) 499-8089

INFORMATION FOR SEQ ID NO: 17:  
 SEQUENCE CHARACTERISTICS:

LENGTH: 822 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-941-445A-17

Query Match 46.7%; Score 2124; DB 3; Length 822;  
 Best Local Similarity 56.1%; Pred. No. 3.4e-198;  
 Matches 389; Conservative 112; Mismatches 167; Indels 26; Gaps 6;

QY 146 IYDIPSLTGRHLDYRYSOYKRLREIDRYEGSLDASRGYKFGFSRSETGYREW 205  
 DB 84 IYDIPSLTGRHLDYRYSOYKRLREIDRYEGSLDASRGYKFGFSRSETGYREW 143  
 QY 206 APGAFWALIGDENNNMADVPMQNEGWEIFLPNNADGSPPIPHGSRVKIMDTPSG 265  
 DB 144 APGAFWALIGDENNNMADVPMQNEGWEIFLPNNADGSPPIPHGSRVKIMDTPSG 202  
 QY 266 NKDSIPAMIKFSVQAPGL--PYNGIYDPPPEEKYFKNPQPKRKSRIYESHVGMSS 323  
 DB 203 NKDSIPAMIKFSVQAPGL--PYNGIYDPPPEEKYFKNPQPKRKSRIYESHVGMSS 262  
 QY 324 TEPVINTYANFRDVLPRIKLGYNAVOLMAIOEHSYASFGYHTNFAAASRGTDPD 383  
 DB 263 TEPVINTYANFRDVLPRIKLGYNAVOLMAIOEHSYASFGYHTNFAAASRGTDPD 322  
 QY 384 LKSLIDKAHEGLVLMDIVHSHASTNTLDGIMFD--GIDGHYFHSGPRGHMMWMSR 440  
 DB 323 LKSLIDKAHEGLVLMDIVHSHASTNTLDGIMFD--GIDGHYFHSGPRGHMMWMSR 382  
 QY 441 LFNYSWELRFLSNARWMLDEYKDFRFDGVTSMYTHHGLOVDTGNTNEXFYAT 500  
 DB 383 LFNYSWELRFLSNARWMLDEYKDFRFDGVTSMYTHHGLOVDTGNTNEXFYAT 442  
 QY 501 DVDAVYIMLNDMHLGFPRAVITIGEYSGMPYVCIYVDEGCVGFYDLRLHMAVADKWE 560

**Tue Aug 7 20:32:51 2001**

us-09-297-703a-29.rai

Page 4

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Db      443  AVDYVVVVVMMMLANLHHKLLLEAFVAVADVDSGMFVLCRPVDEGGGGEFYRLAMAIPRWID  5020
Oy      561  IIOKRD-DWKMGGDIYMHMLNTRNRHLECSVAESHODALVGDGTIAWLMDKMYDFMAL  619
Db      503  YLKKKDDSEWMSGELIATLTNRRYTEKICIVAESHDOSIYGDKLTALLMDKMYGMSD  5620
Oy      620  DRPSTPLIDRVALAHKMTIRLTMLGEGYLNFGNGFNGHPWIDPFRGLHLPSCKEVP  679
Db      563  LQPSAPITDRIALQKMIHFTYMLAGDGYLNFGNGFNGHPWIDPFR-----E  6111
Oy      680  GNNNSYDCRRRFPIDGNSKHLRYHGMOEFDQALQHLAEAGFMTSEHOYISRKDERDRI  7399
Db      612  GNNNSYDCRCRQWSLVTPDHLTRYRYMNAFDQANMALDERSEFLSSKOIYSDMKDEKVL  6711
Oy      740  VFERNGLVFNENFHTSSYSDYRVGCLCPGKXYKIVLSDDPILRGCFRGLSHDAHESEF--  7979
Db      672  VFERNDDLVEFNHFHKRYKIBGKYGKGCOLDPGKIRYALSDALVFGHGRVGHVDHFTSPE  73131
Oy      798  -----EGWYDNRPSREMYTIPCRTPAVYALYALVD  825
Db      732  GVPGVPEETNNRNPRSEKVLSPPRICVATYAYNDE  765

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RESULT 5  
 US-08-104-158-2  
 Sequence 2, Application US/08104158  
 Patent No. 6215042  
 GENERAL INFORMATION:  
 APPLICANT: Willmitzer, Lothar  
 APPLICANT: Sonnenswald, Uwe  
 APPLICANT: Kossmann, Jens  
 APPLICANT: Mueller-Roeder, Bernd  
 APPLICANT: Visser, Richard Gerardus Franciscus  
 APPLICANT: Jacobsen, Evert  
 TITLE OF INVENTION: PLASMIDS CONTAINING DNA-SEQUENCES THAT  
 TITLE OF INVENTION: CAUSE CHANGES IN THE CARBOHYDRATE CONCENTRATION AND THE  
 TITLE OF INVENTION: CARBOHYDRATE COMPOSITION IN PLANTS, AS WELL AS PLANT CELLS  
 TITLE OF INVENTION: AND PLANTS CONTAINING THESE PLASMIDS  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen  
 STREET: 1180 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-8403  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/104,158  
 FILING DATE: 13-AUG-1993  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP PCT/EP92/00302  
 FILING DATE: 11-FEB-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE P 41 04 782.6  
 FILING DATE: 13-FEB-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Melimund, Edward A.  
 REGISTRATION NUMBER: 34,735  
 REFERENCE/DOCKET NUMBER: FR-1996 PCT (951-91)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-382-0700  
 TELEFAX: 212-382-0888  
 TELEX: 236925  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 566 amino acids

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;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-104-158-2

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Query Match	36.0%;	Score 1635.5;	DB 4;	Length 556;
Best Local Similarity	52.2%;	Pred. No. 8.7e-151;		
Matches 316;	Conservative 89;	Mismatches 151;	Indels 19;	Gaps 9;

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0Y 57 SNNWVATSKRVLVLDGRJECYSSSSSTDLAEVIVSESSOVIVDESLLMDCKVYJ3DEYKRA
Db 4 SMDLSTPKSHVRDERMK-HSSAI-----SAYLTB-----DNS 36
0Y 117 ESVPREUVJTRKIGSKPRSLPPGRCORIVDIDPSLTGFRQHLIDRRYSQYKRJREEDJ 176
Db 37 TMAPLEEDVNNENIG-----LNLMDPTLEPYLDHFHRHMKRYVQOKMILEK 82
0Y 177 YEGSLDAESRGYERKFGPGRSETGLTYRPMAGCAFWAALIGFNWNNNAVMOONECW 236
Db 83 YEGPLEEBAOGTLKFGFKREDGCLYTKEMAPADAEVYIGDFNORNSNHMKEDQRCW 142
0Y 237 EFLDPMNADGSPRLPHGSRAKIRMDTPSGN-KDSIPAMIKFSVAQBEFL--PYN3IYDP 293
Db 143 STRIP-DVDSKRVIPHNRSVRKFKHCGWVWDRIPAITKATADATKPAAPDGYWDP 204
0Y 294 PEEERYVKNPDKPRKRLRYTESHVNGSSTEPYINTYANERDDVLERIKKLGYNVOLA 353
Db 202 PSEYEHKRYPPRPAPRIPRYEIAHVNGSSSEPRNYSREPADVDYPRIKANNNTYOLA 261
0Y 354 ATOESHYVAFGYVHTNYTAAVSREGTQDDDLKSLDKNHEGLLVLMIDYVHSHASTYLD 413
Db 262 ALMHSTYSGFEGYHVTNFPFAVSNRNGNEDLKYLLDKNHSGLVLVDVYVHSHASNVD 324
0Y 414 GJNMND---GTGCHYFHSGPRGHHMMWPSRLFNCGSWELRFLLSNARWYLDKXKFGGR 470
Db 322 GJNMNDIGOGSGBSEFPHAGERYHKLMSRLFNANMVEVLRFLLSNLRWLEBYNPDGFR 381
0Y 471 FPGVTSNMTYHHGLDVTGATNEFGYATVDVAVYUMLLMDIHGIFRPAVYIGSEVS 530
Db 382 FPGTISMLTVHNGHJMGSTGANTFSEATIDVAVYUMLLNNLHKIFRPAVYIADVS 444
0Y 531 GMYTCIPEVDGSGEDYRLHMAVADKWEIIO-KREDEMKGIDVIMLITNRKLEKVS 588
Db 442 GMPGSRPSEBEGIDFYRLAMARIDKWDYIKNNNDMDWSMKETSSLTNRRTKECIA 501
0Y 590 YAESHOALVYGKTLTAFWLMDKMDYFALDRSPSTLDRGVALHKKMLRLLTMCIGSEGY 644
Db 502 YAESHOOSIVGKTLTAFLMKENKESGMSCLTDASPVVDAGIADLKMTHIFPNCILGRGV 561
0Y 650 LNFMG 654
Db 562 POEHG 566

```

RESULT 6  
 US-08-528-026C-4  
 : Sequence 4, Application US/08528026C  
 : Patent No. 6248566  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: IMANKA, Tadayuki  
 : APPLICANT: TERADA, Yoshihobu  
 : APPLICANT: TAKARA, Takeshi  
 : APPLICANT: YAMASE, Michiyo  
 : APPLICANT: OKADA, Shigetaka  
 : APPLICANT: TAKATA, Hiroki  
 : APPLICANT: NAKAMURA, Hiroyasu  
 : APPLICANT: FUJII, Kazutoshi  
 :  
 : TITLE OF INVENTION: GLUCAN HAVING CYCLIC STRUCTURE AND METHOD FOR PRODUCING THE  
 :  
 : FURTHER REFERENCE: 9900-0002.20  
 :  
 : CURRENT APPLICATION NUMBER: US/08/528,026C  
 :  
 : CURRENT FILING DATE: 1995-09-13  
 :  
 : PRIOR APPLICATION NUMBER: US 08/415,152  
 :



```

RESULT 7
US-09-187-124-2
; Sequence 2, Application US/09187124A
; Patent No. 625563
;
; GENERAL INFORMATION:
; APPLICANT: Emmermann, Michael
; APPLICANT: Kossmann, Jens
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES CODING FOR DEBRANCHING ENZYMES
; TITLE OF INVENTION: FROM POTATO
; FILE REFERENCE: GFB8

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QY	296	EEKYVKNQOPRPSLSLRYESH-GMSPEPVNTYANRBDV---LPRICKLTVNVO	351
Db	28	EGDILLKFPQ---RDVITYEMHVRGFLPHNSESSTKYPGYIGLYVEKIDHLKELGYNCIE	83
QY	352	LMAIOEHS--YYA-----SFGYHVTFYAASRF-----GTPDDKSL	387
Db	84	LMCEHFEINLEYYSNVSLGYDKFKENMGYSTVNFESPMGRYSAGLSNCGAIINEFYLL	143
QY	388	IDKAHELGLLYLMDIVHSHASTNPLD-LNMEDSTOGHTFHS-GPRGHMMMD--SRLEFN	444
Db	144	VKSAHRGLEGVETMDVFNHHTAEGNENBPILSFRDINSVFYLLAPKGEFYNYSGCGTFEN	203
QY	444	YGSWEVLRPLLSNARWMLDEKFKDFGFRDDGTSAMTYHHGLQVDFGNNEYFGATPVD	503
Db	204	CNNPIYRQETVCLRYWTEBHVNDGFPED-LASIL-----TRSSSMAVNYGNSIDGD	253
QY	504	AV-----VYLLMDIMHGLFPEAVTIGEDVSGMPTVCIPEDGCGVGFDRL---	550
Db	258	MUTTGTPLTSPPLDIMISNDPL-----LSGVKLLAEAMDQGL---YQVGMF	303
QY	551	-HMAVADKKNVELIQKRDDEKMGDVIYHMLTNRMLEKCVSYAESHQDALVGDKT----	604
Db	302	PHMGIMSEW-----NGRYRDMV-----ROFIGTGDFSGAFAECIGSPNLXORG	347
QY	605	-----AFWIMDKMDV-----	615
Db	348	KRPWNSINFCVAHDEFTIADLYTTNNKHNLANGEDKNKDENHNNSMNCGESECFASITVK	407
QY	616	-----FMALDRPSTPLIDRGVALHKKMLRLITMGJGEGYINFMQNEGRCHPEWIDF	665
Db	408	KLRKROMRNFECL- -MVSGCV- -	444
QY	666	PRGDLHLSGKFEVPGNNTSYDKCRRF-----DLGNSHLRYHG-MQDFQALQHL	715
Db	441	-----GGNNNTY--CHDNTYNFRWDKDESSDFLRFCCGIMTKFRHECSL	485
QY	716	EEAYGPMTSE-----HOYISRK--DEEDRIIYVE-----RGLNVYEVN	751
Db	486	GLDEPTAERLQWGHTRPRDMSSESRVAATLVYDKVAGGELYIAFN	532

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RESULT      8
US-08-961-083-80
/ Sequence 80, Application US/08961083
/ Patent No. 6159469
/ GENERAL INFORMATION:
/ APPLICANT: Choi et. al.
/ TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
/ NUMBER OF SEQUENCES: 452
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Human Genome Sciences, Inc.
/ STREET: 9410 Key West Avenue
/ CITY: Rockville
/ STATE: Maryland

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Tue Aug 7 20:32:51 2001

us-09-297-703a-29.ra1

Page 6

COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961,083  
FILING DATE:  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PB340P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ. ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 325 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-961-083-80

Query Match 5.0%; Score 226; DB 4; Length 325;  
Best Local Similarity 25.2%; Pred. No. 1.3e-13;  
Matches 79; Conservative 44; Mismatches 94; Indels 96; Gaps 14;

QY 388 IDKAEHLGLVLMIDIVSHASTNTLDGLNMFDTGTHYFHSGRGHHMMDSRLFNYSW 447  
DB 3 VEECHTHNIGIVYDMVPHXHTIND-DALAYUDGTPREFEYODHNKANHNGALNFDLGN 61  
QY 448 EVLPELLSNAMWLDKXKPFDFGVTSMWYTHNGLOVET-----GNYNEFGYATDV 502  
DB 62 EVQSFLLSCIKHWIDYVHDSIRYDAVSNMLYLDYD-DAPWTRPKDGNLN-YEGY---- 115  
QY 503 DAVYVIMLNMIGLTPREAVTIGEDVSGMPTVCIPVEDGSGVDYRLHMAVADKWEII 562  
DB 116 ---YFLQRLNVIKLEPRDYVMIAFESSSAIKIKGMKEIGLGFDTK----- 159  
QY 563 QKRDEKMGDIYHMLNRRWLEKCYSAE-----SHDQALYGDKTIAFWLMDKMY-- 614  
DB 160 -----MMNG-----WMNDILRFYEDRPYRKIDENLV--TFSEWYAKENYLL 200  
QY 615 ---DEMAIDRPSRLIDRGVALHKKIRLITMGIGEGY-----L 650  
DB 201 PFSHDEVVHGKSS-----MMHKM-----WGDKTINQFAGLRMLYUQICHPEKKL 244  
QY 651 NFMGNFEGH-BEW 662  
DB 245 LFMGSEYGOFLFW 257

RESULT 9  
US-08-399-646-2  
Sequence 2, Application US/08399646  
Patent No. 5556781  
GENERAL INFORMATION:  
APPLICANT: KUBOTA, Michio  
APPLICANT: TSUSAKI, Keiji  
APPLICANT: HATTORI, Kazuko  
APPLICANT: SUGIMOTO, Toshiyuki  
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND  
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/399,646  
FILING DATE: 07-MAR-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 59834  
FILING DATE: 07-MAR-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 59840  
FILING DATE: 07-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: KUBOTA-5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ. ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 389 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-399-646-2

Query Match 4.9%; Score 224.5; DB 1; Length 519;  
Best Local Similarity 20.3%; Pred. No. 5.1e-13;  
Matches 133; Conservative 90; Mismatches 248; Indels 83; Gaps 29;

QY 216 GFNNMNPADWMTONECGWVEIFLNNADSGPPIPHGRKIRMDTPSG-----N 266  
DB 8 GRPDIAVAPRAGCVTLIAGS--ERYEMGRPRGNGPADGEMWT--AADAPFGADVNYGYLLD 63  
QY 267 KDSIPAMIKFSVOAPGELPYNGIY-----YDPREEKYVFKNPQPKRKSILNIESHWGM 321  
DB 64 GDEIPLPDRPTRRPP-----EGVHALSRFTD--PGANRMQDAGMGREIQGSYVIELHIGT 117  
QY 322 SSTPEPIINTYANPRDVLPRIKKLGYNVAQMAIQEHSYASFGYHVNFYAAISREFTP 381  
DB 118 FTPEGLDLAAG--KLDYLAGLIDFTELLPVANFNGTNHWGYDQWFWFVIEGYGAP 173  
QY 382 DDKSLIDKAEHLGLVLMIDIVSHASTNTLDGLNMFDTGTHYFHSGRGHHMMDSRLFNYSW 447  
DB 174 AAYQRFVDAHAAGLGVLDVYVYNNH-----GPRSNYLPKRGYIKIIEGNTW 221  
QY 436 MMDSRLENTGSMWEVRLFLSNARWLDKXKPFDFGVTSMWYTHNGLOVET-----GNYNEFGYATDV 502  
DB 222 GDSVNLDPGSDHYROYLIDNVAMMLRDYRVGDLRIDAV-----HALKDRRAVHIIEE 274  
QY 496 FGATDVDAVVVYVLMIDIMHGLFPEA-----VTIGEDVSGMPTVCIPVEDGCVV----- 545  
DB 275 FGALAD-----ALSSBGRPLTLIEESDLNPRRLYPRDVNGYSLAGQMS 319  
QY 546 --FDYRLHMAVADKWEIIQKRDEKMGDIYHMLTN-----RMWLEK----- 587  
DB 320 DDHNAHVNVNNGSETGYSDPD---SIGALAKVLRDGFHDSYSSPRGRCHGPRINFS 376  
QY 588 -----VSAESHQALYGDKTIAFWLMDKMYEPM-----LDRPSTPLIDGVALH 634  
DB 377 AVHPALVYCSQNHQ--IGNRATGDRLSQSILPYGSIALAAVLTILGPTPL----- 427

Db 8 GRFIMAPRAGVYTLLAGS--EYEMGRRPGNGPADCEWMT--AADAPTADVDYGYLLD 63

QY 267 KDSIPANIKSVAPGPELPYNGIY-----YDPBEERYKFNQPKRPKRSLIYESHYGM 321

Db 64 GDEIPFDPPTRRPQ-----EGVHALSTRFD--PGAHNRQDQMGQORELQSGVYIELHGT 117

QY 322 SSTPEVNTYANRBDVLRIRIKKIGNAVQMAIOEHSYVAFSGYHNTNFFYAASSRFGTP 381

Db 118 FTBEGTIDAAAG---KLIVYLAGLGIDFTELLPVNAFNGTHMWGVDGYQMPAVHEGYGSP 173

QY 382 DDKSLIDKAEHELGLIVLMDIYHSHASTYTLTDLGMMFGDTGCHYF-HSGP-----RCHHW 435

Db 174 AAYQRVYDAHAAGLGVIODYVYNNH-----GPGSANTLPYRYPYLKKGEGNTW 221

QY 436 MMDSLFNTGSMVEVIRFELLSNARWMLDEKDFGRFDGVTSMATYHHGLQYDFGNVEX 495

Db 222 GDSVNDGCGSDHVRQYIIDNVAMMLRDYRVGLRLDAV-----HALDERAVHILEE 274

QY 496 FGATYDVAVYVYLMMLNDKIHGLEPFA-----VTIGEDVSGMPYCIPEVEDGVG----- 545

Db 275 FGLADP-----ALSEGGRPPLTLAESDLPNRLYRDVONGYGLAGQWS 319

QY 546 --FDYRLHMAVADKWEIIOKDEDMKMGDVLHMLTN-----RWMLEKC----- 587

Db 320 DDFHAAVHANNVSGETTYSDFD--SLGALAKVLRGFFHDGYSFRRRCGRPINES 376

QY 588 -----VSASHDOALVGDKTLAFWMLDKWDVDFMA-----LDRSPRLDRGVALLH 634

Db 377 AVHPAALVYVCSGNHQ--IGNRARGDRLSGSLPYGSLALAVLTLTGFPYPMI----- 427

QY 635 KAIRITLWGLGEGYLVNFMGNEFG-----HPWMIDFPRGDLHLSGKRVPGNNYS 684

Db 428 -----FMGEYGATTPWQFETSHPE-----PELGKATAGRIREFEEMG 466

QY 685 YDKC-----RRRPLGNSK---HLR-----YHGMQEDQAIOLHLEAYGFMISE 725

Db 467 WDPANVPPOPEFTFTSKLPMABASGDHARLLEYRLSLITLRSTPELAR-LGFADTA 525

QY 726 HOYISRKDERDIRIIVFERGNLVFENFMHTSSYSDRYGCLKPKKXKIYDSD 779

Db 526 VEF-----DDARWMLRYMGGQYVYLN-----ADRPISLDRPGT-ALTLAYDD 568

RESULT 11

US-08-961-240-2

Sequence 2, Application US/08961240

Patent No. 5830715

GENERAL INFORMATION:

APPLICANT: KUBOTA, Michio

APPLICANT: TSUSAKI, Keiji

APPLICANT: HATTORI, Kazuko

APPLICANT: SUGIMOTO, Toshiyuki

TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

City: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961,240

FILING DATE: 30-OCT-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/399,646

Tue Aug 7 20:32:51 2001

us-09-297-703a-29.rai

Page 8

FILING DATE: 07-MAR-1995  
APPLICATION NUMBER: JP 59834  
FILING DATE: 07-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 59840  
FILING DATE: 07-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: KUBOTA-5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SRO ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 589 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-961-240-2

Query Match 4.9% Score 224.5; DB 2; Length 589;  
Best Local Similarity 20.3% Pred. No. 5.1e-13;  
Matches 133; Conservative 90; Mismatches 248; Indels 183; Gaps 29;

216 GPNMNNPNADVYQNEGWEIPLPNNADGSPPIPHGSRVYKIRMDTPSG-----N 266  
8 GRPDINAPAGVYTLAAG--ERYEMGRPRGNGPADGEMWT--AADAPTGDVYGYLLD 63  
267 KDSIPAMIKESVQAPGELPYNGIY-----YDPPEEKYVFKNPQPKRKSRIYESHVGM 321  
64 GDEIPLDPRTKROP-----EGVHALSRFTD--PGAHMWDAGMCGRELQSGVITELHIGT 117  
322 SSTEPVINTYANFRDVLPRIKLGTNAVQMAIOHSHYASFGYHVNFEVAAASRFGTP 381  
118 FTPEGTLDAAG--KLDYLAGLIDFIELPYNANFNGTHNMGYDQVQWFAVIEGYGCP 173  
382 DDLKSLIDKAHELGLVLMIDIVHSHASTNTLDGLNFDGTDGHYF--HSGP-----RGHM 435  
174 AAYORFYDAHAAGLGVIDVYVNH--GPGSNVLPRIYGPYLIKHEGNTW 221  
436 MMDSRLEFNYSWEVLRFLLSNARWMLDEYKFDGFRDGYTSMYTHGLQVDFGNTVEY 495  
222 GDSVNLDPGSDHVRQYIILDNVAMMLRDYRVGLRLDAY-----HALKDBRAVHILEE 274  
496 EGYATDVDAVVYLMIDMTHGLFPEA--VTIGEDVSGMPTVCIPVEDGCVG-----545  
275 FGALAD-----ALSSGGRPLTILAESDLNPRLLYPRDVGNGYGLAGQWS 319  
546 --PDYRLHMAVADKWEIIOKREDEKMGDIYHMLTN-----RRLMKC-----587  
320 DDFHNAHVAVSGETGYSDFP--SLGALAKVLRDGFHDSYSSFGRCRHGPRINFS 376  
588 -----VSAESHDAOLVGDKTIAFWMKDYDFMA-----LDRPSTPLIDRGVALH 634  
377 AVHRAALVYGSQNDQ--IGNRATGRLSGSLPYGSIALAAVLLTGPTPM-----427  
635 KAIRLITMGLOGEYLKFMENEG-----HPEWIDFPRGDIHLRSGCFVPGNNYS 684  
428 -----FKGEYQATTPMQFTLSHP-----PELGKATVAGRIREFERRMG 466  
685 YDKC-----RRRDLGNSK--HLR-----YHGQERDQALQHLSEAYGFMTESE 725  
467 WDPAVVPDPODEFTTSKLDMASAGDIARLLELYRSLITLRSPRELAR--LGFADTA 525  
726 HOYISRKDERDRIIVFERGNLVYFNFWHTSSSDYRVGCLKPGKXYIADSD 779  
526 VEF-----DDARMLRYMRGQVYVNLN-----ADRPISIDRFGT--ALLATTD 568

RESULT 12

US-08-605-501-2  
Sequence 2, Application US/08605501  
Patent No. 5834287  
GENERAL INFORMATION:  
APPLICANT: KUBOTA, Michio  
APPLICANT: TSUSAKI, Keiji  
APPLICANT: HATTORI, Kazuko  
APPLICANT: SUGIMOTO, Toshiyuki  
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND  
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEWMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 08/605,501  
FILING DATE: 26-FEB-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/399,646  
FILING DATE: 07-MAR-1995  
APPLICATION NUMBER: JP 59834  
FILING DATE: 07-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 59840  
FILING DATE: 07-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: KUBOTA-5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 589 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-605-501-2

Query Match 4.9% Score 224.5; DB 2; Length 589;  
Best Local Similarity 20.3% Pred. No. 5.1e-13;  
Matches 133; Conservative 90; Mismatches 248; Indels 183; Gaps 29;

216 GPNMNNPNADVYQNEGWEIPLPNNADGSPPIPHGSRVYKIRMDTPSG-----N 266  
8 GRPDINAPAGVYTLAAG--ERYEMGRPRGNGPADGEMWT--AADAPTGDVYGYLLD 63  
267 KDSIPAMIKESVQAPGELPYNGIY-----YDPPEEKYVFKNPQPKRKSRIYESHVGM 321  
64 GDEIPLDPRTKROP-----EGVHALSRFTD--PGAHMWDAGMCGRELQSGVITELHIGT 117  
322 SSTEPVINTYANFRDVLPRIKLGTNAVQMAIOHSHYASFGYHVNFEVAAASRFGTP 381  
118 FTPEGTLDAAG--KLDYLAGLIDFIELPYNANFNGTHNMGYDQVQWFAVIEGYGCP 173  
382 DDLKSLIDKAHELGLVLMIDIVHSHASTNTLDGLNFDGTDGHYF--HSGP-----RGHM 435  
174 AAYORFYDAHAAGLGVIDVYVNH--GPGSNVLPRIYGPYLIKHEGNTW 221  
436 MMDSRLEFNYSWEVLRFLLSNARWMLDEYKFDGFRDGYTSMYTHGLQVDFGNTVEY 495

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Db      222 GDSVNLDPGSDHVRQYILIDNVAAMLRDVRVGLRLDAV-----HALKDERAVHILTEE 274
QY      496 FGATVDVAVVYLLMLNDMIGHLEPEA---VTIGEDVSGMPTVCIPVDGCVG----- 545
Db      275 FGALAD-----ALSSGGRPLLLIAESDLNPNRLLYPRVNYGIGLAGQMS 319
QY      546 --FDYRLHMAVADKWEIIOKDEDMKMGDIYHMLTN-----RWMLEKC----- 587
Db      320 DGFHHAHVNVSGETTYGYSDFD--SLGALAKVLDGDFHHDGYSVSPFRCHGRPIINS 376
QY      588 -----VSASHDQALVGDKTIAFWLMDKMDYDPA-----LDRSTPLIDGVALH 634
Db      377 AVHAPALVVCSONHDQ--IGNRATGDRLSQSLPYGSLAAVLLTLPPTPML----- 427
QY      635 KMRLITMGLGEGYLNFMNGNEG-----HPEWIDFPRGDLHPSGKFPVGNYS 684
Db      428 -----FMGEYCATTPWQFTSHPE---PELGKATAGRIREFEPMG 466
QY      685 YDKC-----RRRFDLGNSK---HLR---YHGMQEPDQAIQHEAVGPMTSE 725
Db      467 WDPVAVPDPDETFETFRSKLDMAEASAGDHARLLELYRSLTLTRSTPELAR-LGFADTA 525
QY      726 HOYISRKDERRIIVFERGNLVFENFHWTSYSDYRVGCLPKGKYIVLSDSD 779
Db      526 VEF---DDDAWMLRYMRGVQVYVLFN-----ADRPISLDRPGT-ALLATDSD 568

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## RESULT 13

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US-08-399-646-12
; Sequence 12, Application US/08399646
; Patent No. 5556781

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; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATTORI, Kazuko
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,646
; FILING DATE: 07-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 59834
; FILING DATE: 07-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 59840
; FILING DATE: 07-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: KUBOTA-5
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELETYPE: 248633
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 596 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-399-646-12

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Query Match 4.9%; Score 224.5; DB 1; Length 596;
Best Local Similarity 20.3%; Pred. No. 5,2e-13;
Matches 133; Conservative 90; Mismatches 248; Indels 183; Gaps 29;

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Db      15 GRFDIMAEAGTVLLAG--ERYEMGRPGNGPADGWMWT--AADAATGADVVDGYLLD 70
QY      267 KDSIPAMIKFSVOAPGELPYNGIY-----YDPEEEKYVFKNPKPKRSRIYESHVGM 321
Db      71 GDEIPDPPTRRQP-----EGVHALSTFD--PGAHKQDAGMOGRLOSGYIELHIGT 124
QY      322 STEPVINTYANFRDVLPRIKLGYNAVQMAIOEHSYASFGYHVTNFAASRRPGT 381
Db      125 FTPEGTDLAAG---KIDYLAGIGIDIELLPVNAFNGTHMGVDGVQWFAVHEGYGP 180
QY      382 DDLKSLIDKAHELGLVLMIDYVHSHASTNTLDGLMFDGDGHF-HSGP-----RGHHW 435
Db      181 AAYQREYDAAHAAGIGYIQDVVYNHL-----GPSGNLYPRYGYPLKHEGNTW 228
QY      436 MMDSRLEFNGYSMEVYLFLLSNARWMLDEYKPGDFRPGVTSMTYTHGLQVDFGNNEY 495
Db      229 GDSVNLDPGSDHVRQYILIDNVAAMLRDVRVGLRLDAV-----HALKDERAVHILTEE 281
QY      496 FGATVDVAVVYLLMLNDMIGHLEPEA---VTIGEDVSGMPTVCIPVEDGCVG----- 545
Db      282 FGALAD-----ALSSGGRPLLLIAESDLNPNRLLYPRVNYGIGLAGQMS 326
QY      546 --FDYRLHMAVADKWEIIOKDEDMKMGDIYHMLTN-----RWMLEKC----- 587
Db      327 DGFHHAHVNVSGETTYGYSDFD--SLGALAKVLDGDFHHDGYSVSPFRCHGRPIINS 383
QY      588 -----VSASHDQALVGDKTIAFWLMDKMDYDPA-----LDRSTPLIDGVALH 634
Db      384 AVHAPALVVCSONHDQ--IGNRATGDRLSQSLPYGSLAAVLLTLPPTPML----- 434
QY      635 KMRLITMGLGEGYLNFMNGNEG-----HPEWIDFPRGDLHPSGKFPVGNYS 684
Db      435 -----FMGEYCATTPWQFTSHPE---PELGKATAGRIREFEPMG 473
QY      685 YDKC-----RRRFDLGNSK---HLR---YHGMQEPDQAIQHEAVGPMTSE 725
Db      474 WDPVAVPDPDETFETFRSKLDMAEASAGDHARLLELYRSLTLTRSTPELAR-LGFADTA 532
QY      726 HOYISRKDERRIIVFERGNLVFENFHWTSYSDYRVGCLPKGKYIVLSDSD 779
Db      533 VEF---DDDAWMLRYMRGVQVYVLFN-----ADRPISLDRPGT-ALLATDSD 575

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## RESULT 14

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US-08-607-321-12
; Sequence 12, Application US/08607321
; Patent No. 5716813

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; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HATTORI, Kazuko
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA

```

ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/607,321  
FILING DATE: 26-FEB-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/399,646  
FILING DATE: 07-MAR-1995  
APPLICATION NUMBER: JP 59834  
FILING DATE: 07-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 59840  
FILING DATE: 07-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: KUBOTA-5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 596 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-607-321-12

Query Match 4.9%; Score 224.5; DB 1; Length 596;  
Best Local Similarity 20.3%; Pred. No. 5,2e-13;  
Matches 133; Conservative 90; Mismatches 248; Indels 183; Gaps 29;

216 GDENNMNNADVQWTEFLPNADGSPRPHGSRVIRMDTPSG-----N 266  
15 GRFDINAPKESVQAPGELPYNGIY-----YDPEEEKYVFNKPKRKRSLRTESHYGM 70  
267 KDSIPAMIKFSVQAPGELPYNGIY-----YDPEEEKYVFNKPKRKRSLRTESHYGM 321  
71 GDETLDPKRRKRP-----EGVHLSRTFD-PCAHNMQDAGWGRELQSGVITLHIGT 124  
322 STEEVINTVYVNFQDVLPRIKKLGYNVAOLMAGIQHSYVSPGYHVTNYAASSRFGTP 381  
125 FTPEGTLDAAAG---KLDYLAGLIDITELLPVNAFNGTHMGVYDGVQWFAVHEGYGGR 180  
382 DDLKSLIDKAHELGLVLMIDIVHSHASTNTLDGLNMDGTDGHYF-HSGP-----RGHHW 435  
181 AAYGRFVDAHAAGAGVYIDVYVYHNL-----GPSGNLPRYGPRLKKGEGNTW 228  
436 KWDRLFNYSWMEVYRFLSNARWMLDEKDFGDFGVTSMTYHGLQVDFGTANTNEY 495  
229 GDSVNLDPGSDHVRQXITLDVNAWMLRDYRVQGLDAV-----HALKQERAVHILEE 281  
496 FGATDVDAVVYLMILNDMIGLFEPA-----VTIGEDVSGMPYICIVPEDGCVG----- 545  
282 FGALAD-----ALSEGGRPILTLAESDLNPRILLYPDVGVYGLAGOWS 326  
546 --FDYRLHMAVADKWEITOKRDEDMKMGDIIVHMLTN-----RRMLEK----- 587  
327 DDFHAAVAVNVSGETTYGSPD---SIGALAKYLROGFFHDSYSSRGRCHRPINF 383  
588 -----SYAESHDQALVGDKTAFWLMKMDKMDENA-----LDSPSTLIDRGVALH 634  
384 AVHRAALVYVCSQNDQ---IGNRATGDRLSQSPLGSLAVALVLTIGFTTML----- 434  
635 KMIRLITMGLGEGYLNMGNEFG-----HPEWIDPRQDLHLPSGKEYVPGNNYS 684

435 YDKC-----RRFPDIGNSK---HLR-----YHGMQFDOALQHLERA:GFTWSE 725  
474 WDAVAVPDQDETFYRSLDMAEASAGDHARLELYRLITLRSTPELAR-JGFADTA 532  
726 HOYISKRDERDRIVYERGNLVFVFNHWTSSYSYDVRCGLKPGYKXIVLSD 779  
533 VER-----DDARWLRYMRGQVYVLF-----ADRPISLDRPT-ALLIAND 575

RESULT 15  
US-08-961-240-12  
Sequence 12, Application US/08961240  
Patent No. 5830715  
GENERAL INFORMATION:  
APPLICANT: KUBOTA, Michio  
APPLICANT: TSUSAKI, Keiji  
APPLICANT: HATTORI, Kazuko  
APPLICANT: SUGIMOTO, Toshiyuki  
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961,240  
FILING DATE: 30-OCT-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/399,646  
FILING DATE: 07-MAR-1995  
APPLICATION NUMBER: JP 59834  
FILING DATE: 07-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 59840  
FILING DATE: 07-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: KUBOTA-5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 596 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-961-240-12

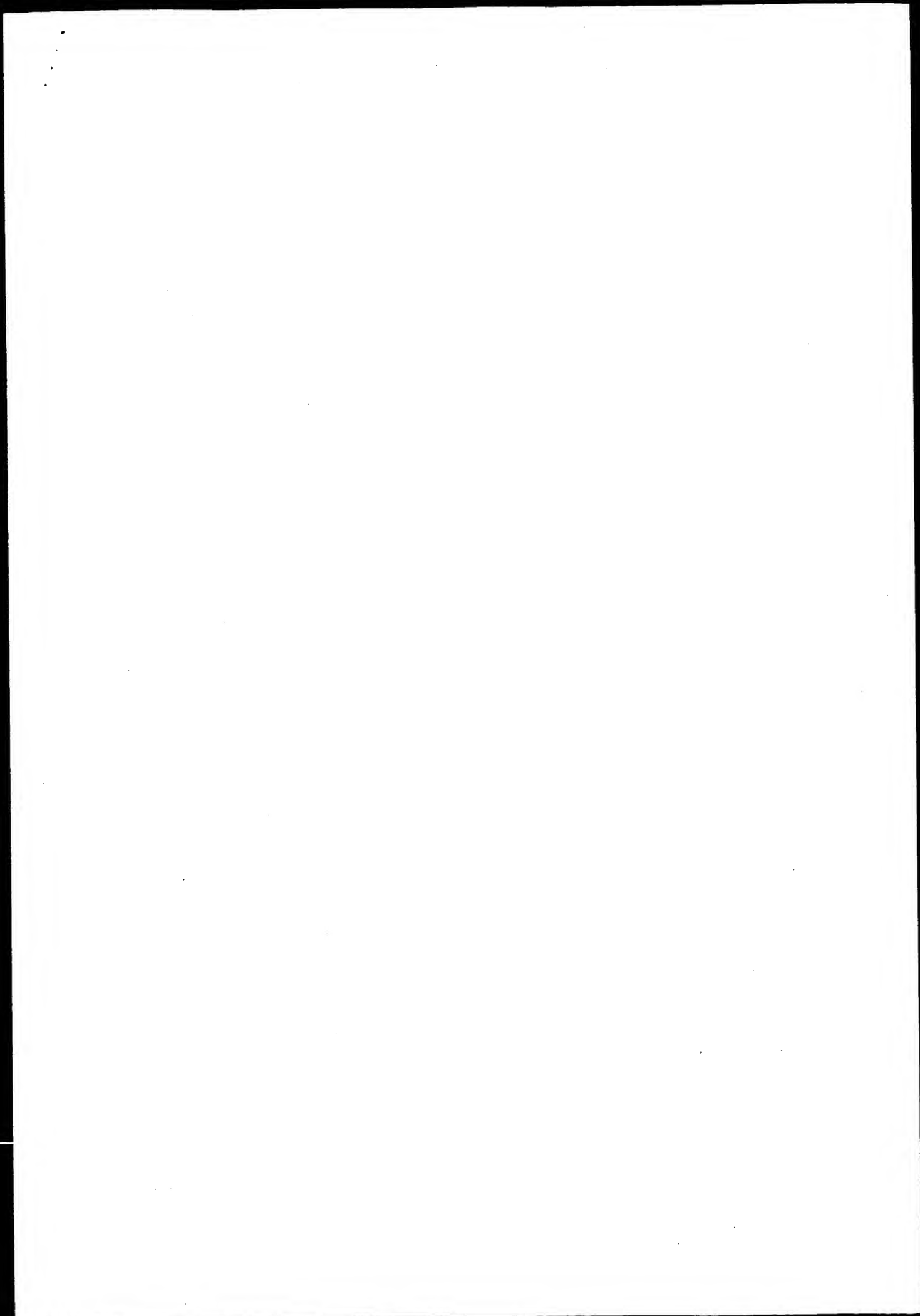
Query Match 4.9%; Score 224.5; DB 2; Length 596;  
Best Local Similarity 20.3%; Pred. No. 5,2e-13;  
Matches 133; Conservative 90; Mismatches 248; Indels 183; Gaps 29;

216 GDENNMNNADVQWTEFLPNADGSPRPHGSRVIRMDTPSG-----N 266  
15 GRFDINAPKESVQAPGELPYNGIY-----YDPEEEKYVFNKPKRKRSLRTESHYGM 70  
267 KDSIPAMIKFSVQAPGELPYNGIY-----YDPEEEKYVFNKPKRKRSLRTESHYGM 321

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Db 71 GDELPDPKRRP-----BGVHALSRTFD-PGAHRWQDAGWQRELOGSVIEYELHGT 124
QY 322 SSTEPVINTYANFRDVLPRIKKIGYNAVOLMAIOEHSYASFGYHVTNFEYAASSRGTP 381
Db 125 FTPEGTIDMAAG-----KIDYIAGIGIDFIELLPYNAENGTHNWGIDGVOWFPAVHEGYGP 180
QY 382 DDLKSLDKAHELILYIMDIIVHSHASTNTLDGLNMFDTGDHYF-HSGP-----RGHHW 435
Db 181 AAYGRFYDAHAAGIGYODVYVNH-----GPSGNVLPYRGPLYKHGEGNTW 228
QY 436 MMDSRLEFNYSWEYLRFLLSARWMLDEYKEDGFRFDGYISMTTHHGLQYDFTGNNEY 495
Db 229 GDSVNLGPGSDHYRQYTLIDVAMMLRDYRVDGLRIDAV-----HALKDERAVHILIE 281
QY 496 FGATFDVAVVYMLLMDMTHGLEPPEA-----VTIGEDVSGMPTVCIPVEDGVG----- 545
Db 282 FGALAD-----ALSSEGGRLVTLAESDLNNRLLYPRDYNGYGLAGQWS 326
QY 546 --FYRLHMAVADKWEVLIQKREDEMKMGDIVHMLN-----RRWLEKC----- 587
Db 327 DDEFHAAVHNVSGETTYSDFD---SLGALAKVLRDGFPHDGSYSFGRCHGRPI NFS 383
QY 588 -----VSYAESHQALVGDKTIAFWLMDKMDWDEMA-----LDRPSTPLIDRGVALH 634
Db 384 AVHRAALVYCSQNHDO--IGNRATGDRLSQSLPFGSLALAVLTLGPFPM----- 434
QY 635 KMIRLITMGLGEGYLNFMGNNEG-----HPEWIDPFRGDLHLPSGKFVPGNNYS 684
Db 435 -----FMGEYGATTPWQFTSHPE-----PELGKATAGRIREFBRMG 473
QY 685 YDKC-----RRPDLGNSK---HLR-----YHGMEFDOAIQHLEAYGEMTSE 725
Db 474 WDPAYVPPDPODPETFRSKLDMAEASAGDHARLELYRSLITLRSTPELAR-LGPAQDTA 532
QY 726 HOYISRKDEDRRIIVEFRGNLVEFNPHTSSYSDYRVGCLKPKXKIYVDSDD 779
Db 533 VEF-----DDARWLRYWRGSGVQVYVNF-----ADRPISIDRPQT-ALLIATDD 575
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Job time: 291 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 7, 2001, 11:17:13 ; Search time 21.07 Seconds  
(without alignments)  
3022.398 Million cell updates/sec

Title: US-09-297-703a-29

Perfect score: 4545  
Sequence: 1 MGHYITSGIRPCAPLCKSQ.....AVYALVEDEVELEPVAG 836

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008

Listing first 45 summaries

Database :

1: p1r:\*  
2: p1r:\*  
3: p1r:\*  
4: p1r:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	3384.5	74.5	800	S65046	1,4-alpha-glucan b
3	3384.5	74.5	805	T48392	1,4-alpha-glucan b
4	3373	74.2	858	B84780	starch branching e
5	3343	73.6	830	T07743	probable 1,4-alpha
6	3327	73.2	854	S65045	1,4-alpha-glucan b
7	3261.5	71.8	814	T02041	1,4-alpha-glucan b
8	3254.5	71.6	823	T06574	probable 1,4-alpha
9	3209	70.6	729	T06797	1,4-alpha-glucan b
10	3180	70.0	825	A48537	1,4-alpha-glucan b
11	3169	69.7	799	T01663	1,4-alpha-glucan b
12	3160	69.5	799	T02981	1,4-alpha-glucan b
13	3160	68.0	830	T07824	1,4-alpha-glucan b
14	2163	47.6	830	T06578	1,4-alpha-glucan b
15	2145	47.2	861	S34730	1,4-alpha-glucan b
16	2130.5	46.9	820	JX0243	1,4-alpha-glucan b
17	2124	46.7	822	JT0968	1,4-alpha-glucan b
18	2072.5	45.6	826	T06494	1,4-alpha-glucan b
19	2049	45.1	702	A46075	1,4-alpha-glucan b
20	1976.5	43.5	702	T49679	1,4-alpha-glucan b
21	1885	41.5	681	T24426	probable branching
22	1765.5	38.8	686	T06334	1,4-alpha-glucan b
23	1487	32.7	704	S50448	1,4-alpha-glucan b
24	1021	22.5	383	S28422	1,4-alpha-glucan b
25	604.5	13.3	774	J00550	1,4-alpha-glucan b
26	591.5	13.0	666	DB2511	1,4-alpha-glucan b
27	587	12.9	770	S76055	hypothetical prote
28	572	12.6	638	S18599	1,4-alpha-glucan b
29	571.5	12.6	630	D70363	1,4-alpha-glucan b

30	571.5	12.6	728	1	NOECA	1,4-alpha-glucan b
31	569.5	12.5	728	2	P86009	1,4-alpha-glucan b
32	566	12.5	730	1	I64118	1,4-alpha-glucan b
33	550.5	12.1	737	2	C81724	1,4-alpha-glucan b
34	550	12.1	705	2	D75345	probable 1,4-alpha
35	542.5	11.9	738	2	A71462	probable glucan b
36	539.5	11.9	666	2	B56639	1,4-alpha-glucan b
37	533.5	11.7	639	1	B41328	1,4-alpha-glucan b
38	524.5	11.5	731	2	B70770	1,4-alpha-glucan b
39	520	11.4	720	2	E72074	1,4-alpha-glucan b
40	520	11.4	720	2	G86549	glucan branching e
41	518.5	11.4	627	1	S40048	1,4-alpha-glucan b
42	517.5	11.4	732	2	H83376	1,4-alpha-glucan b
43	478.5	10.5	764	2	S47569	1,4-alpha-glucan b
44	463.5	10.2	422	2	S31839	1,4-alpha-glucan b
45	462.5	10.2	788	2	S70079	1,4-alpha-glucan b

#### ALIGNMENTS

RESULT	1
T06493	1,4-alpha-glucan branching enzyme (EC 2.4.1.18) I - garden pea
N:Alternate names: starch branching enzyme I	
C:Species: Pisum sativum (garden pea)	
C>Date: 23-Apr-1999 #sequence: revision 23-Apr-1999 #text: change 21-Jul-2000	
C:Accession: T06493	
R:Burton, R.A.; Bewley, J.D.; Smith, A.M.; Bhattacharya, M.K.; Tatge, H.; Ring, S.; Plant J. 7, 3-15, 1995	
A:Title: Starch branching enzymes belonging to distinct enzyme families are different	
A:Reference number: 215717, PMID:95201826	
A:Accession: T06493	
A>Status: preliminary; translated from GB/EMBL/DBJ	
A:Molecule type: mRNA	
A:Residues: 1-922 <BUR>	
A:Cross-references: EMBL:X80009; NID:g510545; PIDN:CA56319.1; PID:g1345570	
C:Genetics:	
A:Gene: SBRI	
C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltr	

Query Match 76.3%; Score 3467; DB 2; Length 922;  
Best Local Similarity 75.6%; Pred No. 2.9e-243;  
Matches 647; Conservative 76; Mismatches 97; Indels 36; Gaps 9;

QY	4	YTISGIRFPCAP-LCKSQSTGFHGYRRTSSCLSF--NFEKAFRRVFSQKSHESDSNV	60
DB	3	YTISGIRFPCAP-LCKSQSTGFHGYRRTSSCLSF--NFEKAFRRVFSQKSHESDSNV	59
QY	61	MYTASRVLDPDGRIEYSSSTQLEAPGVSESOYLIDVESLMD-----	107
DB	60	TIRESDELIPEDQDSVSLIDPDTTSBDAQ--NLEDTLTKDKNKYNIDESTSY	116
QY	108	KIVDE-----VAKESYPMRETV-SIRKIG-SKPRSIIPPGRGORHIDPSLT	154
DB	117	REVGDEKGSVTSLLVDVMTDQAKTSVHSDKKYVDPKRIIPPGRGORHIDPSLT	176
QY	155	GRFOHLDIYRYSQYKRLREIDYKESGLAFSGYKFFSRSRTGITYRENAFATMAAL	214
DB	177	AHQHLDIYRYSQYKRLREIDYKESGLAFSGYKFFSRSRTGITYRENAFATMAAL	236
QY	215	IGDFNNMNNNAVMTQNEGGWEIFLNNAGSPPIPGSRVKIRMPGSPNKSSTPAWI	274
DB	237	VDFNNMNNNAVMTQNEGGWEIFLNNAGSPPIPGSRVKIRMPGSPNKSSTPAWI	296
QY	275	KTSVAPGELPYNGIYDPEEEKYVFNPKPKRSIRIYSHVGSSTPEVINTYANF	334
DB	297	KTSVAPGELPYNGIYDPEEEKYVFNPKPKRSIRIYSHVGSSTPEVINTYANF	356
QY	335	RDDVLPRIKKIGYNAVVOALQEHYVAFSGYHTNTPAASRGITDDDKSLDAKHEL	394

Db 357 RDDVLPRIKKGYNVQJMAIOEHSYASFGYHVNFPAPSSRFGTPEDLKSLIDRAHEL 416  
 QY 395 GLLVMDIVHSHASTNTDGLNMFPGDGHYFHSQPRGHMMHMMBSRLFNYSWEVLRFL 454  
 Db 417 GLLVMDIVHSHASTNTDGLNMFPGDGHYFHSQPRGHMMHMMBSRLFNYSWEVLRFL 476  
 QY 455 SNAKRWLDKXGDEGREGYTSMTYTHGLOVDFTGNANEYFGVATVDVAYVYMLLMDM 514  
 Db 477 SNAKRWLDKXGDEGREGYTSMTYTHGLOVDFTGNANEYFGVATVDVAYVYMLLMDM 536  
 QY 515 INGLEPEAVTIGEDVSGMPTVCIPYEDGCGVDYRLHMAVADKWEIIOKDEDMKMDI 574  
 Db 537 INGLEPEAVTIGEDVSGMPTVCIPYEDGCGVDYRLHMAVADKWEIIOKDEDMKMDI 596  
 QY 575 VMLTNRRMLEKCVSYAESHDQALVGDKTIAFWLMDKMDYMDALDRSTPLIDRGVALH 634  
 Db 597 VMLTNRRMLEKCVSYAESHDQALVGDKTIAFWLMDKMDYMDALDRSTPLIDRGVALH 656  
 QY 635 KMIRLITMGLGEGYLNFMGNFEGHPEDIDPRGDLHPGKFPVGNYSYDKCRREDL 694  
 Db 657 KMIRLITMGLGEGYLNFMGNFEGHPEDIDPRGDLHPGKFPVGNYSYDKCRREDL 716  
 QY 695 GNSKHLRYGMOEFDOAIOHLEAYGFMTSEHQYISRKDERRIIVFERGNLVFVFNH 754  
 Db 717 GNSKHLRYGMOEFDOAIOHLEAYGFMTSEHQYISRKDERRIIVFERGNLVFVFNH 776  
 QY 755 TSQSYRYRGCKLPKRYKIVLSDSDPLFCGFGRLSHDAHFSEFGYDNRPRSFMYVTPC 814  
 Db 777 TSQSYRYRGCKLPKRYKIVLSDSDPLFCGFGRLSHDAHFSEFGYDNRPRSFMYVTPC 836  
 QY 815 RTAVYVAIVEDEYENE 830  
 Db 837 RTAVYVAIVEDEYENE 851

RESULT 2  
 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) isoform SBE2.2 precursor - Arabidopsis thaliana  
 N:Alternate names: starch branching enzyme 2.2  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 22-Nov-1996 #sequence\_revision 22-Nov-1996 #text\_change 18-Jun-1999  
 C:Accession: S65046  
 R:Fishier, D.K.; Gao, M.; Kim, K.N.; Boyer, C.D.; Gultinan, M.J.  
 Plant Mol. Biol. 30, 97-108, 1996  
 A:Title: Two closely related cDNAs encoding starch branching enzyme from Arabidopsis thaliana  
 A:Reference number: S65045; M01D:96197401  
 A:Accession: S65046  
 A:Molecule type: mRNA  
 A:Residues: 1-800 <PI>  
 A:Cross-references: EMBL:U022428; NID:9726489; PIDN:ANB03100.1; PIR:9726490  
 A:Note: only a part of the coding sequence is given  
 C:Genetics:  
 A:Genome: nuclear  
 C:Function:  
 A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-galactosylglucose  
 A:Pathway: glycolysis/starch biosynthesis  
 A:Note: final step in biosynthesis of glycogen or amylopectin  
 C:Superfamily: 1,4-alpha-glucan branching enzyme  
 C:Keywords: chloroplast; glycolysis/starch biosynthesis; glycosyltransferase; hexosyltransferase  
 F:1-40/Domain: trans peptide (chloroplast) #status predicted <TMS>  
 F:41-800/Product: 1,4-alpha-glucan branching enzyme isoform SBE2.2 #status predicted <MA>

Query Match 74.5% Score 3384.5; DB 2: Length 800;  
 Best Local Similarity 75.5% Pred No 2.3e-237;  
 Matches 619; Conservative 80; Mismatches 86; Indels 35; Gaps 8;  
 QY 12 PCADPLCSQSTGFHGYRTSSCLSPNKE-AFSRVSQSGSHSSDSNNVMAASKRVL 70  
 Db 11 PSRPL---NGFNA---GNSLTFPFKRLKRAFGKASAFDSSQALSKSEVL- 62  
 QY 71 DGRTECVSSSTDLQLEAPGVSEE---SQVLTDESLINDKIVEDEYENKESVPMRETVS 126

Db 63 -----VPDNIDDPGFSOLF-DLESQIME---YTEAVRTEDQTIN---V 100  
 QY 127 IRKIGSKPRSIIPPGRGQRIYDIDPSLGEFGHLDYRYSQYKRLREIDKYGSLIDAFSR 186  
 Db 101 VKRGVYPRIVPPGGQKLYEIDPMLRTYNNHLDYRYSQYKRLREIDKYGSLIDAFSR 160  
 QY 187 GYKFGFSRSETGITYREMAPGATMAALLIDENNMPNADVMTQNCQWELFLPNADG 246  
 Db 161 GYKFGFSRSETGITYREMAPGATMAALLIDENNMPNADVMTQNCQWELFLPNADG 220  
 QY 247 SPPLPHSRKIRMDPSPGKSDIPAWIKFSVQAPGELPYNGIYDPPEEKVYVZNPDP 306  
 Db 221 SPPLPHSRKIRMDPSPGKSDIPAWIKFSVQAPGELPYNGIYDPPEEKVYVZNPDP 280  
 QY 307 KRPSKRLIYESHVQMSSTEPVINTYANFRDVLPRIKKLGYNVQJMAIOEHSYASFGY 366  
 Db 281 KRPSKRLIYESHVQMSSTEPVINTYANFRDVLPRIKKLGYNVQJMAIOEHSYASFGY 340  
 QY 367 HTNFEVAASSRFPDPLKSLIDRAHELGLVLMIDIVHSHASTNTDGLNMFPGDGHYF 426  
 Db 341 HTNFEVAASSRFPDPLKSLIDRAHELGLVLMIDIVHSHASTNTDGLNMFPGDGHYF 400  
 QY 427 HSGRGHMMHMMBSRLFNYSWEVLRFLSNARWLDKXGDEGREGYTSMTYTHGLOV 486  
 Db 401 HSGRGHMMHMMBSRLFNYSWEVLRFLSNARWLDKXGDEGREGYTSMTYTHGLOV 460  
 QY 487 DFTGNANEYFGVATVDVAYVYMLLMDKMDYMDALDRSTPLIDRGVALH 546  
 Db 461 DFTGNANEYFGVATVDVAYVYMLLMDKMDYMDALDRSTPLIDRGVALH 520  
 QY 547 DYRLHMAVADKWEIIOKDEDMKMDYMDALDRSTPLIDRGVALH 606  
 Db 521 DYRLHMAVADKWEIIOKDEDMKMDYMDALDRSTPLIDRGVALH 580  
 QY 607 WLMKMDYMDALDRSTPLIDRGVALH 666  
 Db 581 WLMKMDYMDALDRSTPLIDRGVALH 640  
 QY 667 RGDDLPLPGKTFVPGNNYSYDKCRREDIDGNSKHLRYGMOEFDOAIOHLEAYGFMTSE 726  
 Db 641 RGDDLPLPGKTFVPGNNYSYDKCRREDIDGNSKHLRYGMOEFDOAIOHLEAYGFMTSE 700  
 QY 727 QYISRKDERRIIVFERGNLVFVFNHWTSSYSDYRVGCLKPGKRYKIVLSDSDPLFCGFG 786  
 Db 701 QYISRKDERRIIVFERGNLVFVFNHWTSSYSDYRVGCLKPGKRYKIVLSDSDPLFCGFG 760  
 QY 787 RLSHDAHFSEFGYDNRPRSFMYVTPCRTAVYVAIVEDE 826  
 Db 761 RLSHDAHFSEFGYDNRPRSFMYVTPCRTAVYVAIVEDE 800

RESULT 3  
 1,4-alpha-glucan branching enzyme protein isoform SBE2.2 precursor - Arabidopsis thaliana  
 N:Alternate names: protein F17C15.70  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jun-2000  
 C:Accession: T48392  
 R:Bevan, M.; Poll, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, A.  
 submitted to the Protein Sequence Database, March 2000  
 A:Reference number: T48392  
 A:Accession: T48392  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-805 <BEV>  
 A:Cross-references: EMBL:AL162506  
 A:Experimental source: cultivar Columbia; BAC clone F17C15  
 C:Genetics:  
 A:Map position: 5  
 A:Introns: 42/1; 81/3; 142/2; 189/3; 209/3; 236/3; 275/3; 303/3; 344/2; 384/2;  
 A:Note: F17C15.70  
 C:Superfamily: 1,4-alpha-glucan branching enzyme





[illegible]

RESULT 7  
T02041  
1,4-alpha-glucan branching enzyme (EC 2.4.1.18) I1a - maize (fragment)  
N:Alternate names: starch branching enzyme I1a  
C:Species: Zea mays (maize)  
C:Date: 26-Feb-1999 #sequence\_revision 26-Feb-1999 #text\_change 18-Jun-1999  
C:Accession: T02041  
R:Gao, M.; Fisher, D.K.; Kim, K.N.; Shannon, J.C.; Gultinan, M.J.  
Plant Physiol. 114, 69-78, 1997  
A:Title: Independent genetic control of maize starch-branching enzymes I1a and I1b. ISO  
A:Reference number: Z14509; MUID:97303618  
A:Accession: T02041  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-814 <G>  
A:Cross-references: EMBL:U065948; NID:q2340107; PIDN:AA667316.1; PID:q2340108  
A:Experimental source: strain B73  
C:Genetics:  
A:Gene: Sbe2a  
C:Function:  
A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-glucopyranosyl  
C:Superfamily: 1,4-alpha-glucan branching enzyme  
A:Pathway: glycogen/starch biosynthesis  
C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

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Query Match 71.8%; Score 3261.5; DB 2; Length 814;
Best Local Similarity 74.0%; Pred. No. 2e-228;
Matches 604; Conservative 70; Mismatches 109; Indels 33; Gaps 5

QY 36 FNFKEAFSRRV-----GKSHEDSDSNVMTASKRV-----LPDGRICCYSSST-81
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 7 FRRKQAFSTVLSCACAPKVLPPGGSDLLSSAPVVDQPELQIDPAELTVKETS 66
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 82 DLEAFGVTSSESOVLTVYESLIMDK-----VEDEVKESVPARETVSIRKIGS 132
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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D	b	67	SPQTTSVAVMAESSVEAEEREPELSEVIGVGGTGTGKIDAGIKAKAPLVE-----E	118
Q	y	133	KPRSTIPPGRQORIVDDPSLTFGRQHLDIRYQYKRLREEDTKEGSDASRQYERKG	192
D	b	119	KPRVPPPGDQORLEYEIDPMLEGGFHLDYRSEYKRLRALAIDQEHGGDASRQYERKG	178
Q	y	193	FSRSTGTGYEEMAGATWALIGDENMNPADVMTQECGWELPELPNNADGSPPIH	252
D	b	179	FTRSAGELTYREMAAGAAALVGFNMNPNPADAMARNEGVMWELPELPNNADGSPALPH	238
Q	y	253	GSRYATIRMDTFESGNDSITPAMIKFSVOAPGELPYNGIYYDPPEEEKYVKNPOPKRKS	312
D	b	239	GSRYATIRMDTFESGNDSITPAMIKFSVOAPGELPYNGIYYDPPEEEKYVKNPOPKRKS	298
Q	y	313	RIYESHVGMSSTEPYINTYANFRDVLPRIKKLYANAVOLMAIOEHSYASGCHVNTNF	372
D	b	299	RIYESHVGMSSPEPKINTYANFRDEVLPRIKKLYANAVOIMAOEHSYASGCHVNTNF	358
Q	y	373	LAASSRFGTPDDKSLIDKRAHEGLLVMDIVASHASTNTLDLNMFGDGGDGYHFGSPRG	432
D	b	359	APSSRFGTPDDKSLIDKRAHEGLLVMDIVASHSSNNTLDLNGDGDGYHFGSPRG	418
Q	y	433	HHMMDSRLFNYSMEVLEFLLSNARWMLDEKPKGFRPDGYTSMNYTHNHGLQVFTGNV	492
D	b	419	HHMMDSRLFNYSMEVLEFLLSNARWMLDEKPKGFRPDGYTSMNYTHNHGLQVFTGNV	478
Q	y	493	NEYFGATDVDAVVYLLMLNDMIHGLFPEAVTIGEDVSGMPTVCIPVEDGGVGFRLHM	552
D	b	479	GEYFGFATDVDAVVYLLMLNDLIRGLYPEAVSIGEDVSGMPTFCIPVODGGVGFDYRLHM	538
Q	y	553	AVADKMWELIQKRDDEMKKGLVHMLTNRWMLKCYVASYESHDOALVSKTALFMYLMDND	612
D	b	539	AVPDWMIELKOSDEWEGGDIVHLTNTRWMLKCYTYESHDOALVSKTALFMYLMDND	598
Q	y	613	MYDFMALDPSRPLIDRGVALHKMILIRLIMGLEGEGYLFNFMNENFGHPMIDFPRGDLH	672
D	b	599	MYDFMALDPSRPLIDRGVALHKMILIRLIMGLEGEGYLFNFMNENFGHPMIDFPRGDLH	658
Q	y	673	PSGKEVPGNNYSYDKCRRRPDLGNSKHLRYHGMQEFDOALQHLLEAYGPMTSEHOYISRK	732
D	b	659	PNGSYVLPNNNSNFDCCRFRFDELGDADYLRGMQEFDOALQHLLEAYGPMTSEHOYISRK	718
Q	y	733	DERDRIRYERGNLVFVFNFMHTSSYSDVRVCCIKRGKTIYLDSDPLFEGGGRLSHHA	792
D	b	719	HEEDRYIIFERDVLVFNFMHWSNSYFDYVCGCFKRGKTIYLDSDPLFEGGGRSLDHDA	778
Q	y	793	EHFSFEGWTDNPRSFMYVYTPCCTAAVYAL--VEDE 826	
D	b	779	EYFTADMPHDNRPCFSYVAFPSKTAVVYAPAGADE 814	

RESULT 8  
T06574  
probable 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) II precursor - wheat  
C:Species: Triticum aestivum (common wheat)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 20-Jun-2000  
C:Accession: T06574  
R:Chibbar, R.N.  
submitted to the EMBL Data Library, August 1997  
A:Reference number: Z15769  
A:Accession: T06574  
A:Status: translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-823 <CH1>  
A:Cross-References: EMBL:Y11282; PIDN:CAAT2154.1  
A:Experimental source: cv. Fielder; kernels 12 days post anthesis  
C:Genetics:  
A:Gene: sbe2  
C:Function:  
A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha  
A:Pathway: glycogen/starch biosynthesis  
C:Superfamily: 1,4-alpha-glucan branching enzyme  
C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

F:1-54/Domain: transit peptide (amyloplast) #status predicted <NP>  
F:55-823/Product: 1,4-alpha-glucan branching enzyme II #status predicted <MAT>

Query Match 71.6%; Score 3254.5; DB 2; Length 823;  
Best Local Similarity 74.9%; Pred. No. 6,5e-228;  
Matches 590; Conservative 84; Mismatches 89; Indels 25; Gaps 6;

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54 ESDSNVAVTAS-----KRVLPDGRIECYSSSTDLQAFAGVSESQVLTVESLMD---106
55 KSDSRRAVLSSRAAPKGLVVDG-----ESDLSAPAQ-PEELQIPEDIEEGTAEVNM 95
107 -----DKIVEEVK-----ESYPMHEVYSIRK--IGSPRSRIPPGRQRIYDIDPSLTGF 156
96 TGTAEKLESESEPVGIVETITDGTGKGLVGVKELVGVKPRVYKPGDGQKITEIDPTLKDF 155
157 RQHLDIYRISQYKRLREIDIKESGLAPSRQYKGFSPRSSTGITYREMAPGATMAALIG 216
156 RSHLDYRISYRIRRAIDQHEGGLAFSRQYKELGFTSAEGITTYREMAPGASHALVG 215
217 DFNMMNPADVMTONECGVWEIFLPNNADGSPRIPHSRKYKIRMDTPSGNKDISIPAWIKF 276
216 DFNMMNPADVMTONECGVWEIFLPNNADGSPRIPHSRKYKIRMDTPSGNKDISIPAWIKF 275
277 SVQAPGELPYNGIYDPEPEEKYVFNKDPKRPKSLRIYSHVQMSSTPEVITNTANFRD 336
276 SVQAPGELPYNGIYDPEPEEKYVFNKDPKRPKSLRIYSHVQMSSTPEVITNTANFRD 335
337 DVLPRIKLGYNNAVQMAIOEHSYASFGYHVTNFEYAASSRFGPPDLSLIDKAHELGL 396
336 DVLPRIKLGYNNAVQMAIOEHSYASFGYHVTNFEYAASSRFGPPDLSLIDKAHELGL 395
397 LVLMDDYHSHASTWTLDGLMFGDGTGHYHSGRGHHMMWDSRLPYGSMWEYLRRLSN 456
396 LVLMDDYHSHASTWTLDGLMFGDGTGHYHSGRGHHMMWDSRLPYGSMWEYLRRLSN 455
457 ARWLDIEKKGDFGDFGVTSMTYTHHGLQVDFGNYNEGYATDVAVYTLMLDMTH 516
456 ARWLDIEKKGDFGDFGVTSMTYTHHGLQVDFGNYNEGYATDVAVYTLMLDMTH 515
517 GLPFAVITIGEDVSGMPYTCIPVEDGVGFQDYRLHMAVADKWEILIOKREDEKMGDIYH 576
516 GLPFAVITIGEDVSGMPYTCIPVEDGVGFQDYRLHMAVADKWEILIOKREDEKMGDIYH 575
577 MLNNRRLKCYVYAESHDQALVGDKTIAFWLMDKMDYDMALDRSTPLIDGVALHKK 636
576 MLNNRRLKCYVYAESHDQALVGDKTIAFWLMDKMDYDMALDRSTPLIDGVALHKK 635
637 IRLTMDLGEGLYLFNMGNEFGHPWIDFPRGDLHLPSGKFGVNNYSYDKCRRRDLGN 696
636 IRLTMDLGEGLYLFNMGNEFGHPWIDFPRGDLHLPSGKFGVNNYSYDKCRRRDLGN 695
697 SKHLRYSGMQEPDOAIQHLLEAYGFMTSYHQYISRKDERIRIYFREGNLVFEFNHMTS 756
696 ADFLRYSGMQEPDOAIQHLLEAYGFMTSYHQYISRKDERIRIYFREGNLVFEFNHMTS 755
757 SYSDRYGCKLPKGRKYKVLSDPPLFGGFGRLSHDAEHSEFGMGYNNRPSSEWYVPPCT 816
756 SFEDRYGCKLPKGRKYKVLSDPPLFGGFGRLSHDAEHSEFGMGYNNRPSSEWYVPPCT 815
817 AVYVAIVE 824
816 AVYVAIVE 823

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RESULT 9  
T06797  
Probable 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) - wheat  
N:Alternate names: 1,4-alpha-D-glucan 6-alpha-D-(1,4)-alpha-D-glucanotransferase  
C:Species: Triticum aestivum (common wheat)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 18-Jun-1999  
C:Accession: T06797  
R:Kroeger, C.; Loerz, H.; Luetticke, S.

submitted to the EMBL Data Library, August 1996  
A:Reference number: Z15822  
A:Accession: T06797  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Accession: 1-729 <KRO>  
A:Cross-references: EMBL:U66376; NID:g1620661; PIDN:AA017086.1; PID:g1620662  
A:Experimental source: cv. Florida; kernels 21 DAP  
A:Function:  
A:Description: converts amylose into amylopectin; catalyzes the formation of 1,6-gluc  
A:Pathway: starch and sucrose metabolism  
C:Superfamily: 1,4-alpha-glucan branching enzyme  
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 70.6%; Score 3209; DB 2; Length 729;  
Best Local Similarity 78.0%; Pred. No. 1.1e-224;  
Matches 575; Conservative 75; Mismatches 77; Indels 10; Gaps 3;

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88 GTVSESQVLTVESLMDKIVEEVNKESEVPMHEVYSIRKIGSKRPSIPFGGRQRIY 147
89 GTVSESQVLTVESLMDKIVEEVNKESEVPMHEVYSIRKIGSKRPSIPFGGRQRIY 147
3 GGTAEKLESESEPVGIVETITDGTGKGLVGVKELVGVKPRVYKPGDGQKITEIDPTLKDF 52
148 DIDPSLTGFRHLDYRISQYKRLREIDIKESGLAPSRQYKGFSPRSSTGITYREMAP 207
53 EIDPTLKDFRSHLDYRIRYKIRRAIDQHEGGLAFSRQYKELGFTSAEGITTYREMAP 112
208 GATMAALIGDFNNMNPADVMTONECGVWEIFLPNNADGSPRIPHSRKYKIRMDTPSGNK 267
113 GASHALVDEDFNNMNPADVMTONECGVWEIFLPNNADGSPRIPHSRKYKIRMDTPSGNK 172
268 DSIPLAWIKSVQAPGELPYNGIYDPEPEEKYVFNKDPKRPKSLRIYSHVQMSSTPEV 327
173 DSIPLAWIKSVQAPGELPYNGIYDPEPEEKYVFNKDPKRPKSLRIYSHVQMSSTPEV 322
328 INTYANFRDVLPRIKKLGYNNAVQMAIOEHSYASFGYHVTNFEYAASSRFGPPDLSL 387
233 INSTYANFRDVLPRIKKLGYNNAVQMAIOEHSYASFGYHVTNFEYAASSRFGPPDLSL 292
388 IDKAHELGLVLMDDYHSHASTWTLDGLMFGDGTGHYHSGRGHHMMWDSRLPYGSMWEYLRRLSN 447
293 IDKAHELGLVLMDDYHSHASTWTLDGLMFGDGTGHYHSGRGHHMMWDSRLPYGSMWEYLRRLSN 352
448 EYLRRLSNARWMLDEYKDFGDFGVTSMTYTHHGLQVDFGNYNEGYATDVAVYTLMLDMTH 507
353 EYLRRLSNARWMLDEYKDFGDFGVTSMTYTHHGLQVDFGNYNEGYATDVAVYTLMLDMTH 412
508 IMLNDMTHGLPEPAVITIGEDVSGMPYTCIPVEDGVGFQDYRLHMAVADKWEILIOKREDEKMGDIYH 567
413 IMLNDMTHGLPEPAVITIGEDVSGMPYTCIPVEDGVGFQDYRLHMAVADKWEILIOKREDEKMGDIYH 472
568 DPKMGDIYHMLNNRRLKCYVYAESHDQALVGDKTIAFWLMDKMDYDMALDRSTPLIDGVALHKK 627
473 DPKMGDIYHMLNNRRLKCYVYAESHDQALVGDKTIAFWLMDKMDYDMALDRSTPLIDGVALHKK 532
628 DRGVALHKKIRLITLTKKMKLEKCYVYAESHDQALVGDKTIAFWLMDKMDYDMALDRSTPLIDGVALHKK 687
533 DRGVALHKKIRLITLTKKMKLEKCYVYAESHDQALVGDKTIAFWLMDKMDYDMALDRSTPLIDGVALHKK 592
688 CRRRFDLGNKSLRIRHNGQEPDOAIQHLLEAYGFMTSYHQYISRKDERIRIYFREGNLVFEFNHMTS 747
593 CRRRFDLGNKSLRIRHNGQEPDOAIQHLLEAYGFMTSYHQYISRKDERIRIYFREGNLVFEFNHMTS 742
748 FVFNHMTSSYSDYRVGCKLPKGRKYKVLSDPPLFGGFGRLSHDAEHSEFGMGYNNRPSSEWYVPPCT 807
653 FVFNHMTSSYSDYRVGCKLPKGRKYKVLSDPPLFGGFGRLSHDAEHSEFGMGYNNRPSSEWYVPPCT 712
808 FVFNHMTSSYSDYRVGCKLPKGRKYKVLSDPPLFGGFGRLSHDAEHSEFGMGYNNRPSSEWYVPPCT 824
713 FVFNHMTSSYSDYRVGCKLPKGRKYKVLSDPPLFGGFGRLSHDAEHSEFGMGYNNRPSSEWYVPPCT 729

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RESULT 10



A48537  
 starch branching enzyme isoform RBE3 - rice  
 C:Species: Oryza sativa (rice)  
 C>Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 20-Jun-2000  
 C:Accession: A48537  
 R: Mizuno, K.; Kawasaki, T.; Shimada, H.; Satoh, H.; Kobayashi, E.; Okumura, S.; Arai, Y.  
 J. Biol. Chem. 268, 19084-19091, 1993  
 A:Title: Alteration of the structural properties of starch components by the lack of an  
 A:Reference number: A48537; MUID:93366833  
 A:Accession: A48537  
 A:Status: preliminary  
 A:Molecule type: mRNA; protein  
 A:Residues: 1-825 <MTZ>  
 A:Cross-references: GB:D16201; NID:g4336051; PIDN:BA03738.1; PID:g4336052  
 A:Experimental source: cv. Kinmaze  
 A>Note: Sequence extracted from NCBI backbone (NCBI:136747, NCBI:136748)  
 C:Superfamily: 1.4-alpha-glucan branching enzyme

Query Match Best Local Similarity 70.08; Score 3180; DB 2; Length 825;  
 Matches 586; Conservative 87; Mismatches 116; Indels 44; Gaps 7;  
 9 IRPCAPLCKSQSTGFHGRRTSCLSFNFKAFRRVFGSKSHESDSNNWYATAS--- 65  
 20 VRFPV-----PAGASWRAAAELPT--SRLLSGRRPFAVRGSGGGAARVRAAGAS 70  
 66 -KRVLPGRLE--CYSSSTDLEAPGVSE-----ESQVLTDESILMDKIVE 111  
 71 GEVMIPEGESGMPVSAAGSDILQPLADDELSTREVEAGEVEISSGASDVEGV---KRV 126  
 112 DEVKESVPRREYISIKKISKRSPTRPGRGRIYDIDPSLTGFQHLIDYRSQYKRLR 171  
 127 EELAAE-----QKPRVVPPTGDKIFQMDSMNGYXYHLEERYSLYRRLR 172  
 172 EEIDKYGSLDAESRGYKFGFSGRSETGITYREMAPGATWALLIGPFNNWNNADVMTON 231  
 173 SDIDYEGLETFERSRGYKFGFSGRSETGITYREMAPGATWALLIGPFNNWNNADVMTON 232  
 232 ECGWELFLPNNAADGSPTRPHGSRVIRKMDTPSGNKDSTIPAMIKFSVOAGELPYNGITY 291  
 233 EFGWELFLPNNAADGSPTRPHGSRVIRKMDTPSGNKDSTIPAMIKFSVOAGELPYNGITY 292  
 292 DPEEEKYVFNKQPKRPSLRITYESHVGMSSTPEYINTYANFRDYLPRIKKLGYNVAVQ 351  
 293 DPEEEKYVFNKQPKRPSLRITYESHVGMSSTPEYINTYANFRDYLPRIKKLGYNVAVQ 352  
 352 LMAIOEHSTYASFGYVNTNFYAASSRFGTDDLSLIDKAHGLGLVLMIVHSHASTNT 411  
 353 LMAIOEHSTYASFGYVNTNFYAASSRFGTDDLSLIDKAHGLGLVLMIVHSHASTNT 412  
 412 LDGLNFDGTHYFHSRGHMMWDSRLFYNGSWEVLRFLLSNARWMLDEYKFGDFR 471  
 413 LDGLNFDGTHYFHSRGHMMWDSRLFYNGSWEVLRFLLSNARWMLDEYKFGDFR 472  
 472 DGVTSMTYTHHGLOVDFNTNNEYFGYATDVAVVYLMILNDMIGLPEPEAVTTGGEVDSG 531  
 473 DGVTSMTYTHHGLOVDFNTNNEYFGYATDVAVVYLMILNDMIGLPEPEAVTTGGEVDSG 532  
 532 MPVVCIPVEDGAVGPDYRLHMAVADKWEITIOKRDENKMGDIYHMLTNRMLEKCVSYA 591  
 533 MPVVCIPVEDGAVGPDYRLHMAVADKWEITIOKRDENKMGDIYHMLTNRMLEKCVSYA 592  
 592 ESHDQALVADKTIATWLMKDMDYDPMALDRPSTPLIDGVALHMKIRLITMGLEGSEYLN 651  
 593 ESHDQALVADKTIATWLMKDMDYDPMALDRPSTPLIDGVALHMKIRLITMGLEGSEYLN 652  
 652 FNGNFGHPEWIDPFRGDIHLPSGKFPVGNVSYDKCRRRDLGNSKRLRHGQEOEQA 711  
 653 FNGNFGHPEWIDPFRGDIHLPSGKFPVGNVSYDKCRRRDLGNSKRLRHGQEOEQA 712  
 712 IOHLEAVGFPMSEHOYISRKDEDRITVFERGALVYFVNFHMTSSYSDYRVGCLRGKY 771

DB 713 MOSLEKYGFMTSDHOYISRKDEDRITVFERGALVYFVNFHMTSSYSDYRVGCLRGKY 772  
 QY 772 KIVLSDDFLPGEGFGRSLSHDAEHFSEFGWYDNRDRSPMYVTPCARTAVYALVE 824  
 DB 773 KIVLSDDFLPGEGFGRSLSHDAEHFSEFGWYDNRDRSPMYVTPCARTAVYALVE 825  
 RESULT 11  
 1.4-alpha-glucan branching enzyme (EC 2.4.1.18) IIB - maize  
 N:Alternate names: starch branching enzyme IIB  
 C:Species: Zea mays (maize)  
 C>Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 18-Jun-1999  
 R:Kin, K.N.; Fisher, D.K.; Gao, M.; Guiltinan, M.J.  
 Submitted to the EMBL Data Library, June 1998  
 A:Description: Molecular cloning and characterization of the amylose-extender gene en  
 A:Reference number: 214387  
 A:Accession: T01663  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Residues: 1-799 <KIM>  
 A:Cross-references: EMBL:AE072725; NID:g3511235; PIDN:AAC33764.1; PID:g3511236  
 A:Experimental source: strain B73  
 A:Genetics:  
 A:Gene: ae  
 A:Insertions: 38/1; 86/3; 138/2; 171/2; 185/3; 205/3; 232/3; 271/3; 299/3; 340/2; 380/2;  
 A:Function:  
 A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-  
 A:Pathway: glycogen/starch biosynthesis  
 C:Superfamily: 1.4-alpha-glucan branching enzyme  
 C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match Best Local Similarity 69.7%; Score 3169; DB 2; Length 799;  
 Matches 584; Conservative 84; Mismatches 93; Indels 68; Gaps 8;  
 2 GHYISGIRPCAPLCKSQSTGFHGRRTSCLSFNFKAFRRVFGSKSHESDSNNWYATAS--- 61  
 33 GLFLTRARARGC-----SGTHGAMRAA-----AAARKA-----VM 62  
 62 VTASKRVLPDG---RIECYSSSTDLEAPGVSESOV---LTDESILMDKIVEDEVN 115  
 DB 63 VPEGEN---DGLASRADSAQFOGDELEVP-DISEFTGAGAGVADQAL----- 106  
 QY 116 KESVPRREYISIKKISKRSPTRPGRGRIYDIDPSLTGFQHLIDYRSQYKRLREID 175  
 DB 107 -----NRRVVPPTGDKIFQMDSMNGYXYHLEERYSLYRRLRISDID 150  
 QY 176 KYBGSLEDAESRGYKFGFSGRSETGITYREMAPGATWALLIGPFNNWNNADVMONCGV 235  
 DB 151 EHBGGLFARSRSEYKFGFSGRSETGITYREMAPGATWALLIGPFNNWNNADVMONCGV 210  
 QY 236 WEFLFLPNNAADGSPTRPHGSRVIRKMDTPSGNKDSTIPAMIKFSVOAGELPYNGITYDPE 295  
 DB 211 WEFLFLPNNAADGSPTRPHGSRVIRKMDTPSGNKDSTIPAMIKFSVOAGELPYNGITYDPE 270  
 QY 296 EEEYVFNKQPKRPSLRITYESHVGMSSTPEYINTYANFRDYLPRIKKLGYNVAVQ 355  
 DB 271 EKYVFNKQPKRPSLRITYESHVGMSSTPEYINTYANFRDYLPRIKKLGYNVAVQ 330  
 QY 356 QEHSTYASFGYVNTNFYAASSRFGTDDLSLIDKAHGLGLVLMIVHSHASTNTDGL 415  
 DB 331 QEHSTYASFGYVNTNFYAASSRFGTDDLSLIDKAHGLGLVLMIVHSHASTNTDGL 390  
 QY 416 NMFDTGTHYFHSRGHMMWDSRLFYNGSWEVLRFLLSNARWMLDEYKFGDFRQGV 475  
 DB 391 NMFDTGTHYFHSRGHMMWDSRLFYNGSWEVLRFLLSNARWMLDEYKFGDFRQGV 450  
 QY 476 SMYTHHGLOVDFNTNNEYFGYATDVAVVYLMILNDMIGLPEPEAVTTGGEVDSGMPV 535  
 DB 451 SMYTHHGLOVDFNTNNEYFGYATDVAVVYLMILNDMIGLPEPEAVTTGGEVDSGMPV 510

QY 536 CIPVEDGCVGFEDYRLHMAVADKWEIIOKREDEKMGDIYHMLTNRWLEKCVSAESHD 595  
 Db 511 ALPHADGCVGFEDYRLHMAVADKWEIIOKREDEKMGDIYHMLTNRWLEKCVSAESHD 570  
 QY 596 QALVGDGTIAFWLMDKMDYDPMALDRPSTPLIDRGVALHMKMIRLITMGIGEGYLFNMG 655  
 Db 571 QALVGDGTIAFWLMDKMDYDPMALDRPSTPLIDRGVALHMKMIRLITMGIGEGYLFNMG 630  
 QY 656 EFGHEWIDFPRGDLHLPSCGFVPCNNYSYDKCRRRFDLGSKHLRYHGMQEPDQAOIHL 715  
 Db 631 EFGHEWIDFPRGDLHLPSCGFVPCNNYSYDKCRRRFDLGSKHLRYHGMQEPDQAOIHL 690  
 QY 716 EAVGPMTESEHOYISRKDEDRITVEERGNLVFVFNHMTSSYSYRVGCLPKGKYIVL 775  
 Db 691 EAVGPMTESEHOYISRKDEDRITVEERGNLVFVFNHMTSSYSYRVGCLPKGKYIVL 750  
 QY 776 DSDPLNGCGRGLSHDAEHSPFEGWYDNRPSFVYTPCPTAVYALVE 824  
 Db 751 DSDPLNGCGRGLSHDAEHSPFEGWYDNRPSFVYTPCPTAVYALVE 799

## RESULT 12

1.4-alpha-glucan branching enzyme (EC 2.4.1.18) II - maize  
 A:Accession: T02981  
 C:Species: Zea mays (maize)  
 C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 18-Jun-1999  
 C:Accession: T02981  
 R:Khoshooodi, J.; Boyer, C.D.; Hannah, L.C.  
 Plant Physiol. 102, 1045-1046, 1993  
 A:Title: Starch branching enzyme II from maize endosperm.  
 A:Reference number: 214808; MUID:94105320  
 A:Accession: T02981  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-799 <FIS>  
 A:Cross-references: EMBL:L08065; NID:q168482; PIDN:AA18571.1; PID:q168483  
 A:Experimental source: cultivar W64x182E  
 C:Function:  
 A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-g  
 A:Pathway: glycogen/starch biosynthesis  
 C:Superfamily: 1,4-alpha-glucan branching enzyme  
 C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 69.5%; Score 3160; DB 2; Length 799;  
 Best Local Similarity 70.3%; Pred. No. 4,4e-221;  
 Matches 583; Conservative 83; Mismatches 95; Indels 68; Gaps 8;

QY 2 GHYISGIRPCAPDLCKSOSTGFHGYRRTSSCLSFNKEAFSRVSGKSSHSDSNYM 61  
 Db 33 GLFLTRGARVGC-----SGTHGAMRAA-----AAAKA-----YH 62  
 QY 62 VTASKRVLPDG--RIECYSSSTDQLEAPCTVEESQV---LNDVESLMDKIVDEVN 115  
 Db 63 VPBEEN--GGLASRAQSFQSDLEVP--DISEITCGAGVADAQL----- 106  
 QY 116 KEVPMRETVSIRKTSKPSRIPPGRGORITDIPSLTGFROHLYRYOYKRLREID 175  
 Db 107 -----NKRVRPPSPDOCKIFQIDPMLQCKHLEKRYSLYRIRSDID 150  
 QY 176 KYEGLDAFSGYKEFGFSNSETGITREMAFGATMAALIGDFNNMNDVTONCGV 235  
 Db 151 EHEGLEAFSSHYERKFGNASAGITIREMAFGAFSAALVQDVNNMNDVTONCGV 210  
 QY 236 WEIFLPNADGSPPIPHGSRVKTINOTPSGKSDISPAWIKFSVOAPELLYNGITYPPE 295  
 Db 211 WEIFLPNADGSPPIPHGSRVKTINOTPSGKSDISPAWIKFSVOAPELLYNGITYPPE 270  
 QY 296 EEKTVFKPQKRRKSLRTYSHYGMSTEPVINTYANERDDVLPRIKKIGYNVAVOLAI 355  
 Db 271 EEKTVFKPQKRRKSLRTYSHYGMSTEPVINTYANERDDVLPRIKKIGYNVAVOLAI 330

QY 356 QESHYASFGYHVTNFAASSRFGPDDIKSLIDKAHELGLLVMDIYHSAHSTLNDL 415  
 Db 331 QESHYASFGYHVTNFAASSRFGPDDIKSLIDKAHELGLLVMDIYHSAHSTLNDL 390  
 QY 416 NMDGDTGHVFNHSPRGHMMWDSRLNTGSEVYLRELLSNARWMLDEKFGFPFDGVT 475  
 Db 391 NMDGDTGHVFNHSPRGHMMWDSRLNTGSEVYLRELLSNARWMLDEKFGFPFDGVT 450  
 QY 476 SMYTHHGLVDTGNYNEFYAYDVAVYTLMLNDPHGLPRAVYIGEDVYGMPTF 535  
 Db 451 SMYTHHGLVDTGNYNEFYAYDVAVYTLMLNDPHGLPRAVYIGEDVYGMPTF 510  
 QY 536 CIPVEDGCVGFEDYRLHMAVADKWEIIOKREDEKMGDIYHMLTNRWLEKCVSAESHD 595  
 Db 511 ALPHADGCVGFEDYRLHMAVADKWEIIOKREDEKMGDIYHMLTNRWLEKCVSAESHD 570  
 QY 596 QALVGDGTIAFWLMDKMDYDPMALDRPSTPLIDRGVALHMKMIRLITMGIGEGYLFNMG 655  
 Db 571 QALVGDGTIAFWLMDKMDYDPMALDRPSTPLIDRGVALHMKMIRLITMGIGEGYLFNMG 630  
 QY 656 EFGHEWIDFPRGDLHLPSCGFVPCNNYSYDKCRRRFDLGSKHLRYHGMQEPDQAOIHL 715  
 Db 631 EFGHEWIDFPRGDLHLPSCGFVPCNNYSYDKCRRRFDLGSKHLRYHGMQEPDQAOIHL 690  
 QY 716 EAVGPMTESEHOYISRKDEDRITVEERGNLVFVFNHMTSSYSYRVGCLPKGKYIVL 775  
 Db 691 EAVGPMTESEHOYISRKDEDRITVEERGNLVFVFNHMTSSYSYRVGCLPKGKYIVL 750  
 QY 776 DSDPLNGCGRGLSHDAEHSPFEGWYDNRPSFVYTPCPTAVYALVE 824  
 Db 751 DSDPLNGCGRGLSHDAEHSPFEGWYDNRPSFVYTPCPTAVYALVE 799

## RESULT 13

1.4-alpha-glucan branching enzyme (EC 2.4.1.18) I (clone sbel7) - potato (fragment)  
 A:Accession: T07824  
 C:Species: Solanum tuberosum (potato)  
 C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 21-Jul-2000  
 C:Accession: T07824  
 R:Khoshooodi, J.; Blenow, A.; Ek, B.; Rask, L.; Larsson, H.  
 Eur. J. Biochem. 242, 148-155, 1996  
 A:Title: The multiple forms of starch branching enzyme I in Solanum tuberosum.  
 A:Reference number: 216155; MUID:97112484  
 A:Accession: T07824  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-830 <KHO>  
 A:Cross-references: EMBL:Y08786; NID:q1621011; PIDN:CAA70038.1; PID:q1621012  
 A:Experimental source: cv. Diamella; cell line Diamella  
 C:Genetics: sbel  
 C:Function:  
 A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-  
 A:Pathway: glycogen/starch biosynthesis  
 C:Superfamily: 1,4-alpha-glucan branching enzyme  
 C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 48.0%; Score 2180; DB 2; Length 830;  
 Best Local Similarity 54.1%; Pred. No. 5.9e-150;  
 Matches 407; Conservative 116; Mismatches 177; Indels 52; Gaps 10;

QY 109 IVEDEVNKKSVMKRETVSIRKTSKPSRIPPGRGORITDIPSLTGFROHLYRYOYKRLREID 168  
 Db 1 VLTDD--NSTMAPLEEDYKTENIG-----LNDPPTLEPFLDHFIRMRKTY 45  
 QY 169 RLREEDKYEGLDAFSGYKEFGFSRSETGITREMAFGATMAALIGDFNNMNDVTONCGV 228  
 Db 46 DOMLLEKYEGLDAFSGYKEFGFSRSETGITREMAFGATMAALIGDFNNMNDVTONCGV 205  
 QY 229 TONECCEWEIFLPNADGSPPIPHGSRVKTINOTPSGKSDISPAWIKFSVOAPELLYNGITYPPE 285  
 Db 211 WEIFLPNADGSPPIPHGSRVKTINOTPSGKSDISPAWIKFSVOAPELLYNGITYPPE 270

Db 106 EKDDGFWMSIRIP-DVDSKPVIPHNSRVKFRKKGNGCWADRIIPAMIKYATADATKFAAP 164  
 QY 286 YNGIYDPEERKYYFKNPQRPKSLRIYESHVGMSTPEYINTYANERDDVLPRIKL 345  
 Db 165 YGVYDWDPPSRHYHFKYRPPKPRAPRIYEAHVGMSSSEPVNRYRERADVDPRITAN 224  
 QY 346 GYNAVOLMAIOHSHYASFGYHVTNFEYASRFPGDPLKSLIDRAHELGLVIMDIYHS 405  
 Db 225 NNTVOLMAIMEHSHYASFGYHVTNFEYASRFPGDPLKSLIDRAHELGLVIMDIYHS 284  
 QY 406 HASTVTDGLNMF--GTDGHYHSGPRGHMMDSRLFNQSGVEYRFLISNARKMLD 462  
 Db 285 HASNVNTOGLNFDIGGQSGEYFLAERGYSIKLMDSRLEFNANVEYRFLISNARKMLD 344  
 QY 463 EKKDFGPRDGVTSMMYTHHGLVDFTGNYNFEYGYANDVAVVYLMNDMIGLPEEA 522  
 Db 345 EYNFGFPRDGVTSMMYTHHGLVDFTGNYNFEYGYANDVAVVYLMNDMIGLPEEA 404  
 QY 523 VYIGEDVSGMPTVCPYVDGSGVGFDRYRLHMAVADKWEVILIO-KREDKMGDIYHMLTNR 581  
 Db 405 TYIADVDVSGMPTVCPYVDGSGVGFDRYRLHMAVADKWEVILIO-KREDKMGDIYHMLTNR 464  
 QY 582 RWLEKCVASVASHDOALVGDKTIAFWLMDKMDYFMDLRSTPLIDRGVALHMKIRLIT 641  
 Db 465 RYTERCIAVASHDOALVGDKTIAFWLMDKMDYFMDLRSTPLIDRGVALHMKIRLIT 524  
 QY 642 MGLGEGEGLNMGNEFGHPEWIDPRDGLHLPSGKFPVGNNSYDKCRREFDGNKHLR 701  
 Db 573 MALGEGEGLNMGNEFGHPEWIDPRDGLHLPSGKFPVGNNSYDKCRREFDGNKHLR 573  
 QY 702 YHMOEFDOALHLEAYVGMTSEHOYISRKDERRIYFERGNLVYFVFNHMTSSYDY 761  
 Db 574 YKFNAPDRANNSIDKESFSLASGQIVSSMDONKVVYFERGDLVYFVFNHMTSSYDY 633  
 QY 762 RVGLCKPGKXYKIVLSDDPLEPGGGRSLSHDAHEFSF-----EGWYDNRPFSFWYTP 813  
 Db 634 KYGCDLPKTKYVALDSDALMFGGHGRVADHDHFTSPGIGVPEYFNPNRPNFSFKVLS 693  
 QY 814 CRTAVVYALVED-----EVENLEPEYA 835  
 Db 694 ARTCVAYYRDERMSETEYOTDIOCSLELPTA 725  
 RESULT 14  
 T06578  
 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) sbel precursor - wheat  
 N:Alternate names: starch branching enzyme I  
 C:Species: Triticum aestivum (common wheat)  
 C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 20-Jun-2000  
 C:Accession: T06578  
 R:Chibbar, R.N.  
 submitted to the EMBL Data Library, April 1997  
 A:Reference number: Z15772  
 A:Accession: T06578  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-830 <CHI>  
 A:Cross-references: EMBL:Y12320; PIDN:CAA72987.1  
 A:Experimental source: cv. Fielder; kernels at 12 days post-anthesis  
 C:Genetics:  
 A:Gene: Sbel  
 C:Function:  
 A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-g  
 A:Pathway: glycogen/starch biosynthesis  
 C:Superfamily: 1,4-alpha-glucan branching enzyme  
 C:Keywords: amyloplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransf  
 F:1-61/Domain1: transit peptide (amyloplast) #status predicted <TNP>  
 F:62-830/Product: 1,4-alpha-glucan branching enzyme sbel #status predicted <MAT>

Query Match 47.6%; Score 2163; DB 2; Length 830;  
 Best Local Similarity 54.8%; Pred. No. 1e-148;  
 Matches 402; Conservative 115; Mismatches 175; Indels 42; Gaps 10;

QY 115 NKSEVPMREYTSIRKIGSKPR-----SIPPEGRQ-RYVDIDPSLTGRQHLIDRYSOYKR 169  
 Db 56 SKFSVPY-----SAPRDYMAAEDGVGLPYDIDPPKAGKEHFYSRMKLYLD 105  
 QY 170 LREEDIDYEGSLDFAFSRGEYKFSRSEGTGYTEWAPAGATMAALIDGFNNMNPNDVMT 229  
 Db 106 QKSHIEKHGEGLEFSGYGLKFGINTENDATVYREMAPALMDQOLIDFNNMNGSGHRMT 165  
 QY 230 QNEGVWEILPNADGSPPIPHGSRVYKIMADYPPSGN-KDISPAMIKFSVQABGL--PY 286  
 Db 166 KDNVGVMSIRI-SHVNKPKPAIPHNSKVKFRFHKRDGLMVDVRVPAWILYATFADSKFGAPY 224  
 QY 287 NGIYDPEERKYYFKNPQRPKSLRIYESHVGMSTPEYINTYANERDDVLPRIKLK 346  
 Db 225 DGVYMDPPSGRYFKPRPRKPRAPRIYEAHVGMSSSEPVNRYRERADVDPRITAN 284  
 QY 347 YNAVOLMAIOHSHYASFGYHVTNFEYASRFPGDPLKSLIDRAHELGLVIMDIYHS 406  
 Db 285 YNTVOLMAIMEHSHYASFGYHVTNFEYASRFPGDPLKSLIDRAHELGLVIMDIYHS 344  
 QY 407 ASTNTLDGLNMF--GTDGHYHSGPRGHMMDSRLFNQSGVEYRFLISNARKMLD 463  
 Db 345 ASSKKTIDGLNGYDVGONTQSYFHTGGRYHKLMDSRLEFNANVEYRFLISNARKMLD 404  
 QY 464 YKFDGFERDGVTSMMYTHHGLVDFTGNYNFEYGYANDVAVVYLMNDMIGLPEEA 523  
 Db 405 FMDGFRDGVTSMMYTHHGLVDFTGNYNFEYGYANDVAVVYLMNDMIGLPEEA 464  
 QY 524 TIEDVSGMPTVCPYVDGSGVGFDRYRLHMAVADKWEVILIO-KREDKMGDIYHMLTNR 582  
 Db 465 VVAEDVSGMPTVCPYVDGSGVGFDRYRLHMAVADKWEVILIO-KREDKMGDIYHMLTNR 524  
 QY 583 WLEKCVASVASHDOALVGDKTIAFWLMDKMDYFMDLRSTPLIDRGVALHMKIRLIT 642  
 Db 525 YTKCIAVASHDOALVGDKTIAFWLMDKMDYFMDLRSTPLIDRGVALHMKIRLIT 584  
 QY 643 GLGEGEGLNMGNEFGHPEWIDPRDGLHLPSGKFPVGNNSYDKCRREFDGNKHLR 702  
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 Db 634 KYMAAPDRANNSIDKESFSLASGQIVSSMDONKVVYFERGDLVYFVFNHMTSSYDY 693  
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 Db 694 VGCDDLPKTKYVALDSDALMFGGHGRVADHDHFTSPGIGVPEYFNPNRPNFSFKVLS 753  
 QY 815 RTAVVYALVEDVE 828  
 Db 754 RTCVAYYRVEEKAE 767  
 RESULT 15  
 S34730  
 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) precursor, amyloplast - potato  
 N:Alternate names: starch branching enzyme  
 C:Species: Solanum tuberosum (potato)  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 07-Dec-1999  
 C:Accession: S34730; S38733; S18594  
 R:Poulissen, P.  
 submitted to the EMBL Data Library, December 1992  
 A:Description: Starch-branching enzyme cDNA from Solanum tuberosum.  
 A:Reference number: S34730  
 A:Accession: S34730  
 A:Molecule type: mRNA  
 A:Residues: 1-861 <POD>  
 A:Cross-references: EMBL:X69805; NID:9396080; PIDN:CAA49463.1; PID:9396081  
 R:Khoshnoodi, J.; Ek, B.; Rask, L.; Larsson, H.  
 FEBS Lett. 332, 132-138, 1993  
 A:Title: Characterization of the 97 and 103 kDa forms of starch branching enzyme from  
 A:Reference number: S38732; M01D:94009663

A:Accession: S38733  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 76-95;236-244, 'X', 246-255;311-329;393-402;515-520;523-529;545-558; 'F', 636-64  
A:Accession: S38732  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 318-492, 'S', 494-538, 'K', 540-550 <KHM>  
R:Kossmann, J.; Visser, R.G.F.; Mueller-Roeber, B.; Willmitzer, L.; Sonnwald, U.  
Mol. Gen. Genet. 230, 39-44, 1991  
A:Title: Cloning and expression analysis of a potato cDNA that encodes branching enzyme;  
A:Reference number: S18594; MUID:92079917  
A:Accession: S18594  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 279-527 <KOS>  
C:Genetics:  
A:Gene: SBE  
A:Genome: nuclear  
C:Function:  
A:Description: catalyzes the transglycosylation of a terminal segment of a 1,4-alpha-D-g  
A:Pathway: glycogen/starch biosynthesis  
A:Note: final step in biosynthesis of glycogen or amylopectin  
C:Superfamily: 1,4-alpha-glucan branching enzyme  
C:Keywords: amyloplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltrans  
F;1-75/Domain: transit peptide (amyloplast) #status predicted <TNP>  
F;76-861/Product: 1,4-alpha-glucan branching enzyme #status experimental <MAT>

Query Match 47.2% Score 2145; DB 1; Length 861;  
Best Local Similarity 51.6% Pred. No. 2,2e-147;  
Matches 411; Conservative 116; Mismatches 183; Indels 86; Gaps 12;  
QY 34 LSFNFK-----EAFSRKPFSGKSSH-----ESDSNNMVTASKR 67  
DB 1 MEINFKVLSKPIRGSPSPSPKVSQASRKIKTFPSOHSIGLKFGSOERSWDLSSTPKSR 60  
QY 68 VLPDGRTECYSSSTDLAEAGTVSESOYLTVESLIMDKIYEDVKNKESYPMRTYSI 127  
DB 61 VRDERK-RK-HSSAI-----SAVLTD-----DNSTMAPLEEDVKT 93  
QY 128 RKIGSKPRSIIPPGRCGRIVYDPSLTGFRHLDYRSQYKRLREBIDKESGLAFSRG 187  
DB 94 ENIG-----LNLDPTELEPYLDHFRHRRKRYVDQKMLEKEGPLEEPAQS 139  
QY 188 YEKFGFSRSEGTITRYEMAPGATMAALIGDPNNMNPADVMTQNECGWEIFLPNNAQS 247  
DB 140 YLKFGFNRDEGCIYRMAAPAOEDEVIYDIPNGMNGSNHMEKDOFGVMSIRP-DVDSK 198  
QY 248 PPIPHGSRVKIRMDTPSGN-KDSIPAMIKFSVOAPGEL--PYNGIYYDPPEEKYVFKNP 304  
DB 199 PVIPIHNSRVKFRFGKGVVWDRIPIAWIKYATADATKFAAPYDGVVWDPPPSERYHEKYP 258  
QY 305 QPKPKSLRIYESHVGSSTPEVINTYANFRDVLPRIKKLGYNVOLAIOEHSYYASF 364  
DB 259 RPKPRAPRIYEAHVGVSSSEPRVNSYREFADVLPRIKANNVTVOLAIMESHYGSP 318  
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DB 319 GYHTNFPFAVSKRGNEPDLKYLIDKASHLSGLQVLYDVVSHASNNVTDGLNGFDIGOS 378  
QY 422 DGHYFHSRGRGHMMWDSRLFNYSWEVLRFLLSNARWMLDEYKDFGRFDGVTSMYTH 481  
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QY 482 HGLQVDFGTGNVNEYFGATVDVAVYLMMLNDMTIGLEPEAVTIGEDVSGMPTVCIYED 541  
DB 439 HGINNGFTGNVNEYFSEATVDVAVYLMMLNDMTIGLEPEAVTIGEDVSGMPTVCIYED 498  
QY 542 GGVGFDYRLHAAVADKWEIIO-KRDEDMKMGDIYHMLITNRWLEKCVSYAESHDQALVG 600  
DB 499 GCGIFDYRLAAMIPDKWIDYIKNRNDEDMKMEVTSITNRRYTEKCIAYAESHDOSIVG 558

QY 601 DKTIAFWIMDKMDYDFMALDRPSTPLIDRGVALHKMIRITMGLSGEGLVNTNGHEFGHP 660  
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QY 661 EWIDFPRGDIHLPSGKFPVGNVSYDKCRRRFDIGNSKHLRYHGMQEPDQAIQHLLEAYG 720  
DB 619 EWIDFPR-----EGNNMSYDKCRROWMLADSEHLRYKFNMAFPRAVNS-JDEKFS 667  
QY 721 FMTSEHGYISRKDERDRIYFEGNLTVEFNFHWTSSYSYDVRGCLKPGKRYKIVJSDDP 780  
DB 668 FLASGRQIVSSMDDDNKVYVFERGDLVYFNFHPRKNTYEGYKVCDDLPGKRYVAJSDAM 727  
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